



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 140014

TO: Andrew D Kosar
Location: rem/3c04/3c18
Art Unit: 1654
Tuesday, December 14, 2004

Case Serial Number: 10/068905

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Kosar,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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STIC-Biotech/ChemLib

140014

mg.

From: Kosar, Andrew**Sent:** Friday, December 10, 2004 10:44 AM**To:** STIC-Biotech/ChemLib**Subject:** 10/068,905RECEIVED
DEC 10 2005
STIC/ChemLib Division
(STIC)

Please search in 10/068,905
SEQ ID NO: 5, 6, 7, 8, and 9.
They are cyclic tetrapeptides.
thank you,
Andrew Kosar

Andrew D. Kosar, Ph.D.
Art Unit 1654
REMSEN 3C04
Mail REMSEN 3C18

(571)272-0913

12/13/04
SAA
DP

12/14/04

12/10/04

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 21:59:41 ; Search time 80 Seconds

(without alignments)
17.936 Million cell updates/sec

Title: US-10-068-905-5

Perfect score: 15

Sequence: 1 GXYY 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1980s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	86.7	4	1	AAP61656
2	13	86.7	4	1	AAP71313
3	13	86.7	4	2	AAR55333
4	13	86.7	4	2	AAR75499
5	13	86.7	4	5	ABP55713
6	13	86.7	4	5	ABP55796
7	13	86.7	4	5	ABG96845
8	13	86.7	4	5	ABG97024
9	13	86.7	4	5	ABG96697
10	13	86.7	4	5	ABP67652
11	13	86.7	4	5	ABP67653
12	13	86.7	4	5	AAR64247
13	13	86.7	4	6	ABJ18638
14	13	86.7	4	6	ABP59243
15	13	86.7	4	7	ADJ81984
16	13	86.7	4	7	ADL98858
17	13	86.7	4	7	ADL98369
18	13	86.7	4	7	ADL98514
19	13	86.7	4	7	ADL98678
20	13	86.7	4	8	ADK42069
21	13	86.7	4	8	ADK42068
22	13	86.7	5	2	AAR43432
23	13	86.7	5	2	AAR56301
24	13	86.7	5	2	AAR56298
25	13	86.7	5	2	AAR72555

ALIGNMENTS

26	13	86.7	5	2	AAR72549	AAR72549	Pertussis
27	13	86.7	5	2	AAR72699	AAR72699	Kappa-cas
28	13	86.7	5	2	AAY41820	AAY41820	Pertussis
29	13	86.7	5	2	AAY41826	AAY41826	Pertussis
30	13	86.7	5	2	AAR95230	AAR95230	PT toxin
31	13	86.7	5	2	AAR95236	AAR95236	PT toxin
32	13	86.7	5	2	AAY43373	AAY43373	Pertussis
33	13	86.7	5	2	AAY43367	AAY43367	Pertussis
34	13	86.7	5	3	AAY44679	AAY44679	Hydropero
35	13	86.7	5	3	AAY68369	AAY68369	Pertussis
36	13	86.7	5	3	AAY68375	AAY68375	Pertussis
37	13	86.7	5	3	AAB08397	AAB08397	Peptide d
38	13	86.7	5	4	AAB66243	AAB66243	B pertuss
39	13	86.7	5	4	AAB66249	AAB66249	B pertuss
40	13	86.7	5	5	ABP67641	ABP67641	Human CD6
41	13	86.7	5	5	ABP67642	ABP67642	Human CD6
42	13	86.7	5	5	AAE16333	AAE16333	N-termina
43	13	86.7	5	5	ABB75621	ABB75621	Anti-RANK
44	13	86.7	5	6	ABJ18639	ABJ18639	ErDB rece
45	13	86.7	5	6	ABP59244	ABP59244	Peptide e

RESULT 1
AAP61656
ID AAP61656 standard; protein; 4 AA.

XX AAP61656;
AC XX
XX
XX 25-MAR-2003 (revised)
DT 03-OCT-2002 (revised)
DT 21-AUG-1991 (first entry)
XX
XX Sequence of peptide which inhibits cyclic-nucleotide independent protein
DE kinase activity and mammalian cell growth.
XX
XX Cell growth inhibitor; tumour cell growth inhibitor.
XX
XX Synthetic.
OS
FH Key
FT Misc-difference 1 Location/Qualifiers
FT FT /label= Carboxybenzoxy-Phe
FT FT Misc-difference 4 /label= Tyr-CH2Cl

XX US4582821-A.
XX 15-APR-1986.
XX
XX 16-NOV-1983; 83US-00552255.
XX PR 16-NOV-1983; 83US-00552255.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Ketner CA, Racker E;
PI
PI
DR WPI, 1986-118872/18.

XX Inhibition of tumour cell growth - using peptide and aminoacid
PT halo:methyl ketone(s).
XX
XX Claim 1; Col 4; 9pp; English.

XX The cpds. of the invention inhibit protein phosphorylation. The inventors
CC claim a process for inhibiting the growth of tumour cells in a medium
CC which comprises contacting the cells with a cpd. of formula (AAP61654-
CC P61661) or a physiologically acceptable salt. (Updated on 03-OCT-2002 to
CC add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 4 AA;
 Query Match 86.7%; Score 13; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 | |
 2 GAY 4

Db 2 GAY 4

RESULT 2
 AAP71313
 ID AAP71313 standard; protein; 4 AA.
 XX
 AC AAP71313;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-MAY-1991 (first entry)
 XX
 DE Peptide component of cpd. for treating picornavirus infections.
 XX
 KM Picornaviridae; poliovirus; rhinovirus; antiviral agent.
 XX
 CS Synthetic.
 XX
 PN US4636492-A.
 XX
 PD 13-JAN-1987.
 XX
 PF 29-AUG-1984; 84US-00645426.
 XX
 PR 29-AUG-1984; 84US-00645426.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Ketner CA, Korant BD;
 XX
 DR WPI; 1987-036897/05.
 XX
 PT Treating picorna-virus infection with peptide halo:methyl ketone cpds. -
 PT esp. for treating polio virus and rhino virus infections.
 XX
 PS Disclosure; Page 4; 10pp; English.
 XX
 CC This peptide is useful as part of a peptide/halo-methyl ketone cpd., for
 CC treating picornavirus, espolio- or rhinovirus infections. It inhibits the
 CC processing of picornavirus capsid proteins by virus encoded proteases.
 CC See AAP71301-12. See also US4652552. (Updated on 25-MAR-2003 to correct
 CC PA field.)
 CC
 SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 | |
 2 GAY 4

Db 2 GAY 4

RESULT 3
 AAR55333
 ID AAR55333 standard; peptide; 4 AA.
 XX
 AC AAR55333;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-JAN-1995 (first entry)
 XX
 DE Inhibitor of tyrosine kinase.
 XX

KM PK; signal transduction; proliferation; cancer; psoriasis; viral;
 KM inflammatory; allergic; cardiovascular; diseases.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 3
 FT /note= "Tyr(2,3,5,6-P4) (D/L)"
 XX
 PN W09411392-A1.
 XX
 PD 26-MAY-1994.
 XX
 PF 03-NOV-1993; 93WO-US010610.
 XX
 PR 06-NOV-1992; 92US-00973136.
 PR 27-OCT-1993; 93US-00139913.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Dobrusin EM, Mcnamara DJ, Fry DW, Singh J;
 XX
 DR WPI; 1994-183419/22.
 XX
 PT New peptide inhibitors of protein tyrosine kinase - contain D-Tyr or
 PT tetrafluoro-Tyr residue, for treating proliferative diseases, viral
 PT infection, inflammation etc.
 XX
 PS Claim 7; Page 36; 44pp; English.
 XX
 CC The sequence is that of a protein tyrosine kinase inhibitor contg. D-Tyr
 CC or tetrafluoro-Tyr residues. The peptide can be used to inhibit TX-
 CC mediated signal transduction and is useful for controlling proliferative
 CC diseases, e.g. cancer, psoriasis and to treat viral, inflammatory,
 CC allergic and cardiovascular diseases. See also AAR55302-39. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 | |
 1 GAY 3

Db 1 GAY 3

RESULT 4
 AAR75499
 ID AAR75499 standard; peptide; 4 AA.
 XX
 AC AAR75499;
 XX
 DT 25-MAR-2003 (revised)
 DT 13-NOV-1995 (first entry)
 XX
 DE C5a receptor-antagonist core tetrapeptide.
 XX
 KM C5a; C5a receptor-antagonist; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 PN W09516033-A1.
 XX
 PD 15-JUN-1995.
 XX
 PF 16-NOV-1994; 94WO-1B000359.
 PR 06-DEC-1993; 93US-00162591.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX

PI Van Oostrum J, Boyar WC, Galakatos NG, Peppard JV;
XX WPI; 1995-224319/29.
XX
XX C5a receptor antagonists having no agonist activity - are used in
PT compns. to treat C5a-mediated diseases and inflammatory conditions.
XX
XX Disclosure; Page 36; 65pp; English.
XX
XX Polypeptide receptor antagonists to C5a contain an essential core
CC tetrapeptide (AAR75498 or AAR75499) or core tripeptide (DGA) which
CC displays C5a blocking activity. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX
SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GXY 3
| |
2 GAY 4
DB

RESULT 5
ABP55713
ID ABP55713 standard; peptide; 4 AA.
XX
XX ABP55713;
AC
XX 25-FEB-2003 (first entry)
DT
XX
XX B15 class I sHLA molecule ligand related peptide #7.
DE
XX
XX HLA ligand; human leukocyte antigen; predictive algorithm; database;
KW MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
XX
XX Synthetic.
OS
XX
XX WO200269198-A2.
PN
XX
XX 06-SEP-2002.
PD
XX
XX 21-FEB-2002; 2002WO-US005298.
PF
XX
XX 21-FEB-2001; 2001US-0270357P.
PR 10-OCT-2001; 2001US-00974366.
PR 18-DEC-2001; 2001US-00022066.
XX
XX (HILD/) HILDEBRAND W H.
PA (PRIL/) PRILLIMAN K R.
PA (HICK/) HICKMAN H D.
XX
XX Hildebrand WH, Prilliman KR, Hickman HD;
PI WPI; 2002-732755/79.
XX
XX
XX Human leukocyte antigen ligand database assembled by producing HLA having
PT loaded ligands, isolating and sequencing loaded ligands to obtain HLA
PT ligand data and populating database in computer system with ligand data.
XX
XX
XX Disclosure; Fig 5; 118pp; English.

XX
XX The present invention describes a human leukocyte antigen (HLA) (e.g.
CC soluble HLA) ligand database assembled by a process which involves
CC providing a computer system capable of storing HLA data as a database,
CC producing HLA having ligands loaded on it, isolating the loaded ligands
CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
CC populating the database with HLA ligand data. Also described: (1)
CC accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
CC system for HLA (e.g. sHLA) ligand database. The database is populated
CC with HLA ligand sequences, motifs, extended motifs, submotifs, ligands

CC unique to infected cells, tumour specific ligands, as well as a
CC collection of current and future developed HLA ligand sequences. The
CC database which contains endogenously bound and loaded ligands facilitates
CC searching of viral, bacterial, tumour or human protein sequences for
CC ligands likely to bind a particular HLA class I or class II protein. The
CC database allows the user to screen an unknown peptide sequence for
CC potential matches with sHLA ligand discrete sequences or sHLA ligand
CC motifs of sequences. Due to the completeness and concentration of sHLA
CC obtained to date, better sequencing data of numerous endogenously loaded
CC HLA ligands is found in the sHLA ligand database, and by comparison of
CC such ligands to each other and to the genomic sequence, better motifs are
CC also found in the sHLA ligand database. ABP55692 to ABP55912 represent
CC amino acid sequences used in the exemplification of the present invention
XX
XX
SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GXY 3
| |
2 GAY 4
DB

RESULT 6
ABP55796
ID ABP55796 standard; peptide; 4 AA.
XX
XX ABP55796;
AC
XX 25-FEB-2003 (first entry)
DT
XX
XX B15 class I sHLA molecule ligand related peptide #90.
DE
XX
XX HLA ligand; human leukocyte antigen; predictive algorithm; database;
KW MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
XX
XX Synthetic.
OS
XX
XX WO200269198-A2.
PN
XX
XX 06-SEP-2002.
PD
XX
XX 21-FEB-2002; 2002WO-US005298.
PF
XX
XX 21-FEB-2001; 2001US-0270357P.
PR 10-OCT-2001; 2001US-00974366.
PR 18-DEC-2001; 2001US-00022066.
XX
XX (HILD/) HILDEBRAND W H.
PA (PRIL/) PRILLIMAN K R.
PA (HICK/) HICKMAN H D.
XX
XX Hildebrand WH, Prilliman KR, Hickman HD;
PI WPI; 2002-732755/79.
XX
XX
XX Human leukocyte antigen ligand database assembled by producing HLA having
PT loaded ligands, isolating and sequencing loaded ligands to obtain HLA
PT ligand data and populating database in computer system with ligand data.
XX
XX
XX Disclosure; Fig 5; 118pp; English.

XX
XX The present invention describes a human leukocyte antigen (HLA) (e.g.
CC soluble HLA) ligand database assembled by a process which involves
CC providing a computer system capable of storing HLA data as a database,
CC producing HLA having ligands loaded on it, isolating the loaded ligands
CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
CC populating the database with HLA ligand data. Also described: (1)
CC accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
CC system for HLA (e.g. sHLA) ligand database. The database is populated
CC with HLA ligand sequences, motifs, extended motifs, submotifs, ligands

CC The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules (sHLA) in cell pham involving amplifying HLA
 CC allelic DNA by PCR using a locus specific primer to produce truncated a
 CC PCR product (PI), inserting PI into mammalian expression vector;
 CC electroporating the plasmid into a host cell; inoculating the cell pham
 CC with the host cell such that cell pham produces sHLA. A multimeric HLA
 CC complex (I) is useful for testing functionality of peptide ligands bound
 CC by at least two soluble HLA molecules. (I) can be tested for its ability
 CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
 CC responses in humans. (I) is useful for studying T cell responses to
 CC pathological conditions such as viral infections and cancer, and for
 CC modulating the human immune system to induce tolerance in autoimmune
 CC diseases. The individual secreted major histocompatibility complex (MHC)
 CC molecules produced are useful for studies of peptide loading (i.e., in
 CC vaccine development) and to the development of diagnostics. With the
 CC secreted MHC molecules, naturally loaded peptides can be eluted from the
 CC assessment of structural and functional impact of HLA class I
 CC polymorphism. The molecules are also useful to generate ligands and hence
 CC related maps from the peptide pools extracted from series of distinct yet
 CC identify potentially shared elements; and characterise the elements
 CC identified to positively or negatively validate the occurrence of
 CC overlapping ligands. The truncated version of (MHC) can be produced in
 CC mammalian or insect/bacterial cells such that milligram or greater
 CC quantities of an individual class I or class II molecule can be obtained.
 CC This sequence represents a HLA (human leukocyte antigen) peptide ligand.

CC Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 2 GAY 4

RESULT 9
 ID ABG96697 standard; peptide; 4 AA.

AC ABG96697;
 DT 16-DEC-2002 (first entry)

DE Human leukocyte antigen (HLA) B15 ligand #120.

KW Soluble human leukocyte antigen; HLA; sHLA; cell pham;
 KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
 KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
 KW major histocompatibility complex; diagnostic development;
 KW HLA class I polymorphism; HLA-B15 allele; ligand.

OS Homo sapiens.

FN WO200262846-A2.

PD 15-AUG-2002.

PF 18-DEC-2001; 2001WO-US049744.

PR 18-DEC-2000; 2000US-0256409P.

PR 18-DEC-2000; 2000US-0256410P.

PR 10-OCT-2001; 2001US-00974366.

PA (HILD/) HILDEBRAND W H.

PI (PRIL/) PRILLMAN K R.

PI Hildebrand WH, Prillman KR;
 DR WPI; 2002-699563/75.

XX Producing soluble human leukocyte antigen (HLA) in cell pham useful for
 PT studies of peptide loading for characterizing human immune responses
 PT involves using HLA allelic cDNA or genomic DNA as starting material.
 XX Disclosure; Fig 26; 300pp; English.

CC The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules (sHLA) in cell pham involving amplifying HLA
 CC allelic DNA by PCR using a locus specific primer to produce truncated a
 CC PCR product (PI), inserting PI into mammalian expression vector;
 CC electroporating the plasmid into a host cell; inoculating the cell pham
 CC with the host cell such that cell pham produces sHLA. A multimeric HLA
 CC complex (I) is useful for testing functionality of peptide ligands bound
 CC by at least two soluble HLA molecules. (I) can be tested for its ability
 CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
 CC responses in humans. (I) is useful for studying T cell responses to
 CC pathological conditions such as viral infections and cancer, and for
 CC modulating the human immune system to induce tolerance in autoimmune
 CC diseases. The individual secreted major histocompatibility complex (MHC)
 CC molecules produced are useful for studies of peptide loading (i.e., in
 CC vaccine development) and to the development of diagnostics. With the
 CC secreted MHC molecules, naturally loaded peptides can be eluted from the
 CC MHC molecule and characterised. The secreted MHC molecules allow the
 CC assessment of structural and functional impact of HLA class I
 CC polymorphism. The molecules are also useful to generate ligands and hence
 CC related maps from the peptide pools extracted from series of distinct yet
 CC identify potentially shared elements; and characterise the elements
 CC identified to positively or negatively validate the occurrence of
 CC overlapping ligands. The truncated version of (MHC) can be produced in
 CC mammalian or insect/bacterial cells such that milligram or greater
 CC quantities of an individual class I or class II molecule can be obtained.
 CC This sequence represents a HLA (human leukocyte antigen) peptide ligand.

CC Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 2 GAY 4

RESULT 10

ID ABP67652 standard; peptide; 4 AA.

AC ABP67652;

DT 10-DEC-2002 (first entry)

DE Human CD66 family modulating peptide SEQ ID NO 523.

KW Human; CD66; CEACAM; cytostatic; antiinflammatory; immunomodulator;
 KW antibacterial; virucide; gene therapy; vaccine; neutrophil;
 KW immune system; autoimmune disease; cancer; infection; bacterial; virus;
 KW inflammatory disease; transplantation; immunisation.

OS Homo sapiens.

FN WO200268601-A2.

PD 06-SEP-2002.

PF 27-FEB-2002; 2002WO-US005720.

PR 28-FEB-2001; 2001US-0272113P.

PA (SKUB/) SKUBITZ K M.
 PI (SKUB/) SKUBITZ A P N.

XX Skubitz KM, Skubitz APN;
 XX WPI; 2002-706981/76.
 DR New peptide from a surface exposed region of a CD66 family member, useful
 PT for modulating the function of CD66 family members, e.g. activation of
 PT neutrophils, for treating or diagnosing autoimmune diseases or cancer,
 PT and as a vaccine.
 XX Claim 2; Page 30; 96pp; English.
 XX The invention relates to an isolated peptide (I) from a surface exposed
 CC region of a CD66 family member (ABP67130-ABP67990). The peptide
 CC modulates: (a) activation of neutrophils; (b) activation or inhibition of
 CC T-cells, B-cells, NK cells, LAK cells, dendritic cells or other immune
 CC system cells; (c) proliferation and/or differentiation of the above
 CC cells, including epithelial cells; (d) homotypic and/or heterotypic
 CC adhesion among CD66 family members; and (e) adhesion of CD66 family
 CC members to other ligands. The peptide is useful in modulating the
 CC function of CD66 family members and/or their ligands, such as activation
 CC of neutrophils and activation, inhibition, proliferation and/or
 CC differentiation of the immune cells. The peptides may also be used in
 CC treating or diagnosing autoimmune diseases, cancer, infections (e.g.
 CC bacterial or viral) or inflammatory diseases, in transplantation
 CC therapies and for immunisation
 CC
 SO Sequence 4 AA;
 SO
 Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 Db 2 GSY 4
 Db
 RESULT 11
 ABB67653
 ID ABB67653 standard; peptide; 4 AA.
 XX
 AC ABB67653;
 XX
 DT 10-DEC-2002 (first entry)
 XX
 DE Human CD66 family modulating peptide SEQ ID NO 524.
 XX
 KW Human; CD66; CEACAM; cytostratic; antiinflammatory; immunomodulator;
 KW antibacterial; virucide; gene therapy; vaccine; neutrophil;
 KW immune system; autoimmune disease; cancer; infection; bacterial; virus;
 KW inflammatory disease; transplantation; immunisation.
 XX
 OS Homo sapiens.
 XX
 PN WO200268601-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 27-FEB-2002; 2002WO-US005720.
 XX
 PR 28-FEB-2001; 2001US-0272113P.
 XX
 PA (SKUB/) SKUBITZ K M.
 PA (SKUB/) SKUBITZ A P N.
 XX
 PI Skubitz KM, Skubitz APN;
 XX
 DR WPI; 2002-706981/76.
 PT New peptide from a surface exposed region of a CD66 family member, useful
 PT for modulating the function of CD66 family members, e.g. activation of
 PT neutrophils, for treating or diagnosing autoimmune diseases or cancer,
 PT and as a vaccine.

PT and as a vaccine.
 XX Claim 2; Page 30; 96pp; English.
 XX The invention relates to an isolated peptide (I) from a surface exposed
 CC region of a CD66 family member (ABP67130-ABP67990). The peptide
 CC modulates: (a) activation of neutrophils; (b) activation or inhibition of
 CC T-cells, B-cells, NK cells, LAK cells, dendritic cells or other immune
 CC system cells; (c) proliferation and/or differentiation of the above
 CC cells, including epithelial cells; (d) homotypic and/or heterotypic
 CC adhesion among CD66 family members; and (e) adhesion of CD66 family
 CC members to other ligands. The peptide is useful in modulating the
 CC function of CD66 family members and/or their ligands, such as activation
 CC of neutrophils and activation, inhibition, proliferation and/or
 CC differentiation of the immune cells. The peptides may also be used in
 CC treating or diagnosing autoimmune diseases, cancer, infections (e.g.
 CC bacterial or viral) or inflammatory diseases, in transplantation
 CC therapies and for immunisation
 CC
 SO Sequence 4 AA;
 SO
 Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 Db 1 GSY 3
 Db
 RESULT 12
 AA084247
 ID AA084247 standard; peptide; 4 AA.
 XX
 AC AA084247;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Caspase cleavage site #11.
 XX
 KW Caspase; apoptosis; GAP SH3 binding protein; HCD2; AOP-1; cancer;
 KW apoptosis-associated disease; hyperproliferative disease; AIDS;
 KW degenerative disease; autoimmune disease; Alzheimer's disease;
 KW viral infection; acquired immunodeficiency syndrome; vascular disease;
 KW myocardial infarction; oxidative stress; ischaemic stroke; arthritis;
 KW heart failure; Parkinson's disease; amyotrophic lateral sclerosis.
 XX
 OS Unidentified.
 XX
 PN WO200196873-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 15-JUN-2001; 2001WO-BP006780.
 XX
 PR 16-JUN-2000; 2000EP-00112813.
 PR 16-NOV-2000; 2000EP-00125013.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Rudel T, Thiede B, Machny N;
 XX
 DR WPI; 2002-098088/13.
 XX
 PT Novel apoptosis-associated and/or -modified protein useful as target for
 PT the diagnosis, prevention or treatment of apoptosis-associated diseases
 PT particularly neurodegenerative diseases.
 XX
 PS Claim 30; Page 62; 86pp; English.
 XX
 CC The invention relates to an apoptosis-associated and/or -modified protein
 CC (I) selected from GAP SH3 binding protein, HCD2 and AOP-1 (not defined)
 CC or its proteolytic fragments. (I) is useful as target for the diagnosis,

CC prevention or treatment of apoptosis-associated diseases, for the
 CC manufacture of a pharmaceutical agent and for identifying apoptosis
 CC modulators. The proteome is useful as a target for the diagnosis,
 CC prevention or treatment of apoptosis-associated diseases, and in a method
 CC for identifying apoptosis modulators. (I) is useful for treatment of
 CC hyperproliferative or degenerative diseases including cancers, autoimmune
 CC diseases, Alzheimer's disease, viral infections such as acquired
 CC immunodeficiency syndrome (AIDS) and vascular diseases such as myocardial
 CC infarction. (I) is also useful for treating and/or preventing diseases
 CC related to oxidative stress like ischemic stroke, arthritis, heart
 CC failure, Parkinson's disease and amyotrophic lateral sclerosis. (I) is
 CC also useful to develop modification-specific diagnostic tools. (I) is
 CC also useful for developing protein chips or other solid phase screening
 CC devices for high throughput screens, and also as a diagnostic tool to
 CC screen for caspase activity, and/or to determine the effectiveness of
 CC caspase cleavage inhibiting and/or modulating substances. A084237-
 CC A084260 represent caspase cleavage sites of the invention

XX Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 | | |
 Db 1 GSY 3

RESULT 13

AB018638
 ID AB018638 standard; peptide; 4 AA.

XX AC AB018638;

XX DT 20-FEB-2003 (first entry)

DE ErbB receptor antagonist peptide #21.

XX KM Vaccine; erbB receptor antagonist; tumour; cancer; gastric cancer;
 KM breast cancer; prostate cancer.

XX OS Unidentified.

XX PN WO200281649-A2.

XX PD 17-OCT-2002.

PF 08-APR-2002; 2002WO-US011211.

PR 06-APR-2001; 2001US-02820372.

PR 03-AUG-2001; 2001US-0309864P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX PI Greene MI, Zhang H, Murali R, Richter M, Berezov A, Liu Q;

XX PI Chen U;

DR WPI; 2003-075482/07.

PT New peptide antagonists against erbB receptors, useful for preventing or
 PT treating tumors or cancers (e.g. lung adenocarcinomas, breast carcinomas
 PT or prostate cancer) in humans.

PS Claim 1, Page 82; 115pp; English.

XX The invention comprises peptide antagonists designed to target erbB
 CC receptors. The erbB receptor peptide antagonists are useful for
 CC preventing tumors and cancers (e.g. gastric cancer, breast cancer and
 CC prostate cancer). The present amino acid sequence represents an erbB
 CC receptor peptide antagonist of the invention

XX Sequence 4 AA;

Query Match 86.7%; Score 13; DB 6; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 | | |
 Db 2 GSY 4

RESULT 14

ABP59243
 ID ABP59243 standard; peptide; 4 AA.

XX AC ABP59243;

XX DT 10-MAY-2003 (first entry)

DE Peptide epitope for generating cell surface receptor antibody, SEQ ID 21.

XX KM Antibody; cytostatic; vaccine; cell surface receptor; erbB; TNF;

XX KM immunoglobulin gene superfamily; IGSF; epitope.

XX OS Synthetic.

XX PN WO2003012072-A2.

XX PD 13-FEB-2003.

PF 05-AUG-2002; 2002WO-US024892.

PR 03-AUG-2001; 2001US-0309864P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX PI Greene MI, Zhang H, Richter M, Murali R;

XX PI WPI; 2003-268117/26.

PT Novel antibody for preventing, treating, imaging or diagnosing tumor, has
 PT specificity for activated cell surface receptor and binds specifically to
 PT an epitope that does not comprise phosphotyrosine residue.

PS Claim 53; Page 88; 114pp; English.

XX The present invention relates to novel antibodies, which have specificity
 CC for activated cell surface receptors (erbB, TNF and immunoglobulin gene
 CC superfamily; IGSF) and bind to an epitope (ABP59223-ABP59259). The
 CC antibodies are useful for preventing transformation of a normal cell into
 CC a tumour cell in a patient who had a tumour with tumour cells that
 CC express activated erbB receptors on the cell surface surgically removed
 CC or in whom the tumour has entered remission, for treating a patient
 CC suffering from a cancer characterised by tumour cells that have p185 on
 CC their cell surfaces, or for treating a patient suffering from an erbB
 CC tumour. The antibodies were produced by immunising a suitable host with a
 CC peptide (ABP59223-ABP59259), or its reverse sequence

XX Sequence 4 AA;

Query Match 86.7%; Score 13; DB 6; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 | | |
 Db 2 GSY 4

RESULT 15

AD081984
 ID AD081984 standard; peptide; 4 AA.

XX AC AD081984;

XX 06-MAY-2004 (first entry)
DT Thermus brockianus nucleic acid polymerase peptide fragment #2.
XX
DE nucleic acid polymerase, thermophile; mutation; exonuclease activity.
XX
KM Thermus brockianus.
XX
OS WO2003048308-A2.
XX
PN 12-JUN-2003.
XX
PD 22-NOV-2002; 2002MO-US037657.
XX
PF 30-NOV-2001; 2001US-0334434P.
XX
PR (APPL-) APPLERA CORP.
XX
PA Rozzelle J, Bolchakova E;
XX
PI WPI; 2003-505285/47.
XX
DR
XX
PT New Thermus brockianus nucleic acid polymerases, useful for DNA
PT synthesis, primer extension, DNA sequencing, reverse transcription, or
PT DNA and RNA amplification procedures.
XX
PS Disclosure; SEQ ID NO 18; 74pp; English.
XX
XX The invention relates to novel nucleic acid polymerases from the
CC thermophilic organism Thermus brockianus or mutants having a mutation
CC that decreases 5'-3' exonuclease activity or reduces discrimination
CC against dideoxynucleotide triphosphates. The nucleic acid polymerases,
CC isolated nucleic acids encoding the polymerases, vectors, host cells and
CC kits are useful for DNA synthesis, primer extension, DNA sequencing,
CC reverse transcription, or DNA and RNA amplification procedures. The
CC nucleic acids are also useful for the recombinant expression of the
CC polymerase polypeptides. The nucleic acid polymerases and nucleic acids
CC are useful for the detection and isolation of nucleic acids encoding DNA
CC polymerase I activity. This sequence corresponds to a peptide of a
CC polymerase of the invention.
XX
SQ Sequence 4 AA;
Query Match 86.7%; Score 13; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GXY 3
| |
| |
Db 1 GAY 3
Search completed: December 13, 2004, 22:22:39
Job time : 83 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:12:37 ; Search time 21.4 seconds
(without alignments)

12.396 Million cell updates/sec

Title: US-10-068-905-5

Perfect score: 15

Sequence: 1 GXXX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA:
2: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	13	86.7	4	1 US-08-798-897-49	Sequence 49, Appl
2	13	86.7	4	1 US-08-463-824-2	Sequence 2, Appl
3	13	86.7	4	2 US-08-463-377-2	Sequence 2, Appl
4	13	86.7	4	2 US-08-978-523-49	Sequence 49, Appl
5	13	86.7	4	2 US-08-310-112A-199	Sequence 199, App
6	13	86.7	4	2 US-09-301-085-199	Sequence 199, App
7	13	86.7	4	5 PCT-US93-01668-41	Sequence 41, Appl
8	13	86.7	4	5 PCT-US93-04589-159	Sequence 159, Appl
9	13	86.7	5	1 US-07-962-569A-6	Sequence 6, Appl
10	13	86.7	5	1 US-08-292-968-30	Sequence 30, Appl
11	13	86.7	5	2 US-08-618-696-3	Sequence 36, Appl
12	13	86.7	5	2 US-08-618-696-3	Sequence 36, Appl
13	13	86.7	5	2 US-08-618-696-3	Sequence 36, Appl
14	13	86.7	5	2 US-08-618-696-3	Sequence 36, Appl
15	13	86.7	5	2 US-08-618-696-3	Sequence 36, Appl
16	13	86.7	5	2 US-08-618-696-3	Sequence 36, Appl
17	13	86.7	5	2 US-08-618-696-3	Sequence 36, Appl
18	13	86.7	5	3 US-09-033-753-3	Sequence 3, Appl
19	13	86.7	5	3 US-09-033-753-3	Sequence 14, Appl
20	13	86.7	5	3 US-08-467-876-36	Sequence 30, Appl
21	13	86.7	5	3 US-08-467-876-36	Sequence 30, Appl
22	13	86.7	5	3 US-09-082-514-30	Sequence 30, Appl
23	13	86.7	5	3 US-09-082-514-30	Sequence 30, Appl
24	13	86.7	5	4 US-08-475-955-143	Sequence 143, Appl
25	13	86.7	6	1 US-08-014-979-92	Sequence 92, Appl
26	13	86.7	6	1 US-08-176-620A-21	Sequence 21, Appl
27	13	86.7	6	1 US-08-248-538-20	Sequence 20, Appl

28	13	86.7	6	1 US-08-248-538-40	Sequence 40, Appl
29	13	86.7	6	1 US-08-260-199A-31	Sequence 31, Appl
30	13	86.7	6	1 US-08-260-199A-32	Sequence 32, Appl
31	13	86.7	6	1 US-08-798-897-53	Sequence 53, Appl
32	13	86.7	6	1 US-08-690-605-21	Sequence 21, Appl
33	13	86.7	6	2 US-08-580-988A-16	Sequence 16, Appl
34	13	86.7	6	2 US-08-461-985-21	Sequence 21, Appl
35	13	86.7	6	2 US-08-978-523-53	Sequence 53, Appl
36	13	86.7	6	3 US-08-481-985B-132	Sequence 132, Appl
37	13	86.7	6	3 US-08-932-787B-12	Sequence 12, Appl
38	13	86.7	6	3 US-08-932-012C-12	Sequence 12, Appl
39	13	86.7	6	3 US-08-888-818C-12	Sequence 12, Appl
40	13	86.7	6	4 US-09-518-737-6	Sequence 6, Appl
41	13	86.7	6	5200320-19	Patent No. 5200320
42	13	86.7	7	1 US-07-841-997A-19	Sequence 19, Appl
43	13	86.7	7	1 US-08-290-101-19	Sequence 19, Appl
44	13	86.7	7	2 US-09-070-756-8	Sequence 8, Appl
45	13	86.7	7	3 US-09-193-104-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-798-897-49
; Sequence 49, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Gaestella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-798-897-49

Query Match 86.7%; Score 13; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GXY 3
DB 2 GAY 4

RESULT 2
US-08-463-224-2
Sequence 2, Application US/08463224
Patent No. 5807824
GENERAL INFORMATION:
APPLICANT: van Oostrum, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5807824agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSES: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463, 224
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-224-2
Query Match 86.7%; Score 13; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GXY 3
DB 2 GAY 4
RESULT 3
US-08-463-377-2
Sequence 2, Application US/08463377
Patent No. 5837499
GENERAL INFORMATION:
APPLICANT: van Oostrum, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5837499agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSES: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463, 377
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-377-2
Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GXY 3
DB 2 GAY 4
RESULT 4
US-08-978-523-49
Sequence 49, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSES: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978, 523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798, 897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Edmund, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483, 0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide.
US-08-978-523-49

Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GAY 4

RESULT 5

US-08-310-912A-199
; Sequence 199, Application US/08310912A
; Patent No. 5981730
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310-912A
; FILING DATE: September 22, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/254001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 199:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-310-912A-199

Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GAY 4

RESULT 6
US-09-301-085-199
; Sequence 199, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/301,085
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-301-085-199

Query Match 86.7%; Score 13; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GAY 4

RESULT 7
PCT-US93-01669-41
; Sequence 41, Application PC/TUS9301669
; GENERAL INFORMATION:
; APPLICANT: Towbridge, Ian S.
; APPLICANT: Collawn, Jr., James F.
; APPLICANT: Tainer, John A.
; APPLICANT: Kuhn, Leslie A.
; TITLE OF INVENTION: RECEPTOR INTERNALIZATION SIGNALS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01669
; FILING DATE: 01-MAR-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/844,852
; FILING DATE: 03-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-1636
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US93-0169-41

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GSY 4

RESULT 8
PCT-US95-04589-199
Sequence 199, Application PC/TUS9504589
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskiewicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katsagiri, Pamiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mandinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04589
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04589-199

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GTY 4

RESULT 9
US-07-962-569A-6
Sequence 6, Application US/07962569A
Patent No. 5351497
GENERAL INFORMATION:
APPLICANT: MENON, RAVI S.
APPLICANT: JEFFERS, KATHLEEN F.
APPLICANT: CHANG, YING-FON
APPLICANT: HAW, RICHARD G.
TITLE OF INVENTION: HUMAN K-CASEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FREDERICK W. PEPPER, PH.D.
STREET: 11545 W. BERNARDO COURT, STE. 302
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92127
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/962,569A
FILING DATE: 19921013
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 920224.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 451-1120
TELEFAX: (619) 451-9628
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-962-569A-6

Query Match 86.7%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 3 GTY 5

RESULT 10
US-08-292-968-30
Sequence 30, Application US/08292968
Patent No. 5856122
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COWEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney

STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-388
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-968-30

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 1 GXY 3
DB 2 GTY 4
RESULT 11
US-08-292-968-36
Sequence 36, Application US/08292968
Patent No. 5856122
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COHEN, Raymond P.
APPLICANT: LOOMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-388
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-968-36
Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 1 GXY 3
DB 2 GTY 4

RESULT 12
US-08-618-696-3
Sequence 3, Application US/08618696
Patent No. 5861475
GENERAL INFORMATION:
APPLICANT: COOPER, Jr., J. ALLEN D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
INHIBITION OF PHAGOCYTES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,696
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,269
FILING DATE: 12/21/92
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 00AB:002/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acid residues
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-618-696-3

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 1 GSY 3

RESULT 13
US-08-618-696-14 Application US/08618696
Sequence 14, Application US/08618696
Patent No. 5861475
GENERAL INFORMATION:
APPLICANT: COOPER, JR., J. ALLEN D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,696
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,269
FILING DATE: 12/21/92
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UOAB:002/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-618-696-14

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 1 GSY 3

RESULT 14
US-08-467-974-30
Sequence 30, Application US/08467974
Patent No. 5965385
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.

APPLICANT: COHEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,974
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-454 MIS.vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-974-30

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 15
US-08-467-974-36
Sequence 36, Application US/08467974
Patent No. 5965385
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COHEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46

Tue Dec 14 10:04:26 2004

us-10-068-905-5.ra1

Page 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,974
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-454 MIS:v9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-974-36

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GTY 4

Search completed: December 13, 2004, 22:34:51
Job time : 22.4 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:31:47 ; Search time 68.6 Seconds
(without alignments)
20.827 Million cell updates/sec

Title: US-10-068-905-5

Perfect score: 15

Sequence: 1 GXVX 4

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 35178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	86.7	4	9 US-09-867-852-199	Sequence 199, App
2	13	86.7	4	14 US-10-302-817A-18	Sequence 18, App
3	13	86.7	4	15 US-10-613-472-199	Sequence 199, App
4	13	86.7	4	16 US-10-613-765-199	Sequence 199, App
5	13	86.7	5	10 US-09-792-686A-34	Sequence 34, App
6	13	86.7	5	14 US-10-344-779-8	Sequence 8, App
7	13	86.7	5	14 US-10-376-121A-143	Sequence 143, App
8	13	86.7	5	16 US-10-738-809-8	Sequence 8, App
9	13	86.7	5	16 US-10-394-471B-3	Sequence 3, App
10	13	86.7	5	16 US-10-394-471B-11	Sequence 11, App
11	13	86.7	6	9 US-09-990-762-36	Sequence 36, App
12	13	86.7	6	9 US-09-990-762-40	Sequence 40, App
13	13	86.7	6	9 US-09-990-762-41	Sequence 41, App

14	13	86.7	6	10 US-09-518-737-6	Sequence 6, App
15	13	86.7	6	10 US-09-858-852A-36	Sequence 36, App
16	13	86.7	6	10 US-09-858-852A-40	Sequence 40, App
17	13	86.7	6	10 US-09-858-852A-41	Sequence 41, App
18	13	86.7	6	14 US-10-285-045-23	Sequence 23, App
19	13	86.7	6	14 US-10-284-660-23	Sequence 23, App
20	13	86.7	6	15 US-10-394-980-232	Sequence 232, App
21	13	86.7	6	15 US-10-306-631-63	Sequence 63, App
22	13	86.7	6	15 US-10-438-751-108	Sequence 108, App
23	13	86.7	6	15 US-10-438-751-121	Sequence 121, App
24	13	86.7	6	15 US-10-133-234A-17	Sequence 17, App
25	13	86.7	6	15 US-10-133-234A-18	Sequence 18, App
26	13	86.7	6	15 US-10-133-234A-19	Sequence 19, App
27	13	86.7	6	15 US-10-133-234A-20	Sequence 20, App
28	13	86.7	6	15 US-10-133-234A-21	Sequence 21, App
29	13	86.7	6	16 US-10-415-014-732	Sequence 732, App
30	13	86.7	6	16 US-10-739-583-14	Sequence 14, App
31	13	86.7	6	17 US-10-813-638-1446	Sequence 1446, App
32	13	86.7	7	9 US-09-809-517A-15	Sequence 15, App
33	13	86.7	7	10 US-09-792-686A-31	Sequence 31, App
34	13	86.7	7	14 US-10-286-457-129	Sequence 129, App
35	13	86.7	7	14 US-10-286-457-189	Sequence 189, App
36	13	86.7	7	15 US-10-398-104-326	Sequence 326, App
37	13	86.7	7	17 US-10-741-481-35	Sequence 35, App
38	13	86.7	8	9 US-09-765-086-157	Sequence 157, App
39	13	86.7	8	9 US-09-756-283A-59	Sequence 59, App
40	13	86.7	8	9 US-09-756-283A-97	Sequence 97, App
41	13	86.7	8	9 US-09-962-445-15	Sequence 15, App
42	13	86.7	8	10 US-09-910-552-22	Sequence 22, App
43	13	86.7	8	10 US-09-880-748-1084	Sequence 1084, App
44	13	86.7	8	14 US-10-264-374-157	Sequence 157, App
45	13	86.7	8	14 US-10-375-992-157	Sequence 157, App

ALIGNMENTS

RESULT 1
US-09-867-852-199
Sequence 199, Application US/09867852
Patent No. US20020147324A1
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Starkawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumitaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
TITLE OF INVENTION: DETECTION METHODS
FILE REFERENCE: 00786/254002
CURRENT APPLICATION NUMBER: US/09/867,852
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 199
LENGTH: 4
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-867-852-199
Query Match 86.7%; Score 13; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 2

US-10-302-817A-18
; Sequence 18, Application US/10302817A
; Publication No. US20030198978A1
; GENERAL INFORMATION:
; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768US
; CURRENT FILING DATE: 2002-11-22
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Thermus brockianus
US-10-302-817A-18

Query Match 86.7%; Score 13; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 1 GTY 3

RESULT 3

US-10-613-472-199
; Sequence 199, Application US/10613472
; Publication No. US20040089756A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumitaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254004
; CURRENT APPLICATION NUMBER: US/10/613,472
; CURRENT FILING DATE: 2003-07-02
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/301,085
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: US 08/310,912
; PRIOR FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: US 08/227,360
; PRIOR FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-472-199

Query Match 86.7%; Score 13; DB 15; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 4

US-10-613-765-199
; Sequence 199, Application US/10613765
; Publication No. US20040172673A1
; GENERAL INFORMATION:
; APPLICANT: AUSUBEL, FREDERICK M.
; APPLICANT: STASKAWICZ, BRIAN J.
; APPLICANT: KATAGIRI, FUMITAKI
; APPLICANT: KUNKEL, BARBARA N.
; APPLICANT: MINDRINOS, MICHAEL N.
; APPLICANT: YU, GUO-LIANG
; APPLICANT: BAKER, BARBARA
; APPLICANT: ELLIS, JEFFREY
; APPLICANT: SALMERON, JOHN
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254005
; CURRENT APPLICATION NUMBER: US/10/613,765
; CURRENT FILING DATE: 2003-07-02
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/301,085
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: US 08/310,912
; PRIOR FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: US 08/227,360
; PRIOR FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-765-199

Query Match 86.7%; Score 13; DB 16; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 5

US-09-792-686A-34
; Sequence 34, Application US/09792686A
; Publication No. US20030068645A1
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Kopecky, Stephen L.
; APPLICANT: Weyand, Cornelia M.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR EVALUATING
; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
; FILE REFERENCE: 07039-250001
; CURRENT APPLICATION NUMBER: US/09/792,686A
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-686A-34

Query Match 86.7%; Score 13; DB 10; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GXY 3
| |
Db 3 GTY 5

RESULT 6
US-10-344-779-8

; Sequence 8, Application US/10344779
; Publication No. US2003021106A1
; GENERAL INFORMATION:
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TORNETTA, MARK A.
; APPLICANT: TRUNER, ALEMSEGED
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
; FILE REFERENCE: GPE0033
; CURRENT APPLICATION NUMBER: US/10/344,779
; PRIOR FILING DATE: 2003-02-17
; PRIOR APPLICATION NUMBER: PCT/US01/26161
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,524
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/230,639
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-344-779-8

Query Match 86.7%; Score 13; DB 14; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GXY 3
| |
Db 1 GTY 3

RESULT 7

US-10-376-121A-143
; Sequence 143, Application US/10776121A
; Publication No. US2003021654A1
; GENERAL INFORMATION:
; APPLICANT: Hatley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Patrea J. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991

; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea J.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRI14CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 143:
US-10-376-121A-143

Query Match 86.7%; Score 13; DB 14; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GXY 3
| |
Db 1 GTY 3

RESULT 8
US-10-738-809-8
; Sequence 8, Application US/10738809
; Publication No. US2004017117A1
; GENERAL INFORMATION:
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TORNETTA, MARK A.
; APPLICANT: TRUNER, ALEMSEGED
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
; FILE REFERENCE: GPE0033
; CURRENT APPLICATION NUMBER: US/10/738,809
; PRIOR FILING DATE: 2003-02-17
; PRIOR APPLICATION NUMBER: US/10/344,779
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US01/26161
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,524
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/230,639
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-738-809-8

Query Match 86.7%; Score 13; DB 16; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GXY 3
| |
Db 1 GTY 3

RESULT 9
US-10-394-471B-3
; Sequence 3, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill; Carton, Jill; Scallion, Bernard J.

FILE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN0202
CURRENT APPLICATION NUMBER: US/10/394,471B
CURRENT FILING DATE: 2003-03-21
CURRENT APPLICATION NUMBER: 60/367,903
PRIOR FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentln Ver 3.1
SEQ ID NO 3
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-10-394-471B-3

Query Match 86.7%; Score 13; DB 16; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
|
|
Db 2 GSY 4

RESULT 10
US-10-394-471B-11
Sequence 11, Application US/10394471B
Publication No. US20040185047A1
GENERAL INFORMATION:
APPLICANT: GILES-KOMAR, JILL; CARTON, JILL; SALLON, BERNARD J.
TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN0202
CURRENT APPLICATION NUMBER: US/10/394,471B
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/367,903
PRIOR FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentln Ver 3.1
SEQ ID NO 11
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-10-394-471B-11

Query Match 86.7%; Score 13; DB 16; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
|
|
Db 2 GSY 4

RESULT 11
US-09-990-762-36
Sequence 36, Application US/09990762
Patent No. US20020119498A1
GENERAL INFORMATION:
APPLICANT: JOUNG, J. KEITH
APPLICANT: MILLER, JEFFREY
APPLICANT: PABO, CARL O.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
FILE REFERENCE: MTV-030.02 (20021-3002)
CURRENT APPLICATION NUMBER: US/09/990,762
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 09/858,852
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/204,509
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 36
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
OTHER INFORMATION: recognition sequence
US-09-990-762-36

Query Match 86.7%; Score 13; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
|
|
Db 3 GAY 5

RESULT 12
US-09-990-762-40
Sequence 40, Application US/09990762
Patent No. US20020119498A1
GENERAL INFORMATION:
APPLICANT: JOUNG, J. KEITH
APPLICANT: MILLER, JEFFREY
APPLICANT: PABO, CARL O.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
FILE REFERENCE: MTV-030.02 (20021-3002)
CURRENT APPLICATION NUMBER: US/09/990,762
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 09/858,852
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/204,509
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 40
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
OTHER INFORMATION: recognition sequence
US-09-990-762-40

Query Match 86.7%; Score 13; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
|
|
Db 3 GAY 5

RESULT 13
US-09-990-762-41
Sequence 41, Application US/09990762
Patent No. US20020119498A1
GENERAL INFORMATION:
APPLICANT: JOUNG, J. KEITH
APPLICANT: MILLER, JEFFREY
APPLICANT: PABO, CARL O.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
FILE REFERENCE: MTV-030.02 (20021-3002)
CURRENT APPLICATION NUMBER: US/09/990,762
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 09/858,852
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/204,509
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 41
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-990-762-41

Query Match
Best Local Similarity 86.7%; Score 13; DB 9; Length 6;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 3 GAY 5

RESULT 14
US-09-518-737-6
; Sequence 6, Application US/09518737
; Publication No. US2003008321A1
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHISA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; PRIOR APPLICATION NUMBER: 2000-03-03
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-6

Query Match
Best Local Similarity 86.7%; Score 13; DB 10; Length 6;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 4 GSY 6

RESULT 15
US-09-858-852A-36
; Sequence 36, Application US/09858852A
; Publication No. US20030044787A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTX-030.01 (20021-3001)
; CURRENT APPLICATION NUMBER: US/09/858,852A
; PRIOR APPLICATION NUMBER: 2001-05-16
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-858-852A-36

Query Match 86.7%; Score 13; DB 10; Length 6;

Best Local Similarity 86.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 3 GAY 5

Search completed: December 13, 2004, 23:02:39
Job time : 69.6 secs

This Page Blank (uspto)

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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:01:21 ; Search time 15.2 Seconds
(without alignments)
25.320 Million cell updates/sec

Title: US-10-068-905-5

Perfect score: 15

Sequence: 1 GXYX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	86.7	9	2	S36850
2	13	86.7	9	2	G41946
3	13	86.7	11	2	PT0250
4	13	86.7	11	2	PT0214
5	13	86.7	12	2	A33099
6	13	86.7	12	2	S47391
7	13	86.7	12	2	S47395
8	13	86.7	12	2	PH1611
9	13	86.7	12	2	PH0882
10	13	86.7	12	2	PH0790
11	13	86.7	13	2	S47383
12	13	86.7	13	2	PH0788
13	13	86.7	13	2	PH0788
14	13	86.7	13	2	PH0788
15	13	86.7	14	2	AS9018
16	13	86.7	14	2	PH1601
17	13	86.7	14	2	PH0792
18	13	86.7	15	2	PH1582
19	13	86.7	16	2	S11290
20	13	86.7	17	2	S48655
21	13	86.7	17	2	A60317
22	13	86.7	17	2	F35141
23	13	86.7	18	2	T73024
24	13	86.7	18	2	PH1629
25	13	86.7	19	2	PH1609
26	13	86.7	20	2	FX0059
27	13	86.7	20	2	JA0142
28	13	86.7	20	2	AS4519
29	13	86.7	20	2	PL0161

30	13	86.7	20	2	S44465
31	13	86.7	21	2	PT0227
32	13	86.7	21	2	S47198
33	13	86.7	21	2	S47212
34	13	86.7	22	2	PH1680
35	13	86.7	22	2	AS3794
36	13	86.7	23	2	AS3631
37	13	86.7	23	2	PH1725
38	13	86.7	24	2	I73584
39	13	86.7	24	2	I61491
40	13	86.7	24	2	D27579
41	13	86.7	24	2	A05298
42	13	86.7	24	2	E45087
43	13	86.7	24	2	S56000
44	13	86.7	25	2	AS8647
45	13	86.7	26	2	P00105

ALIGNMENTS

RESULT 1

Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999

C/Accession: S36850

R/Jacob, J.; Kelsoe, G.

submitted to the EMBL Data Library, July 1992

A/Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophen

A/Reference number: S25024

A/Accession: S36850

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-9 <JAC>

A/Cross-references: EMBL:X67387; NID:950113; PIDN:CAA47799.1; PID:es1594; PID:g1333871

C/Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 86.7%; Score 13; DB 2; Length 9;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3

DB 6 GSY 8

RESULT 2

T-cell receptor gamma chain (2t.23) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C/Accession: G41946

R/Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A/Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma g

A/Reference number: A11946; MUID:92049316; PMID:1658619

A/Accession: G41946

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-9 <WHE>

C/Keywords: T-cell receptor

Query Match Best Local Similarity 86.7%; Score 13; DB 2; Length 9;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3

DB 3 GSY 5

RESULT 3

PT0250
 Ig heavy chain CRD3 region (clone 2-109B) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0250
 R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Share, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A/Reference number: PT0222; MUID:91108337; PMID:1899102
 A/Accession: PT0250
 A/Molecule type: DNA
 A/Residues: 1-11 <YAM>
 A/Experimental source: B lymphocyte
 C/Keywords: heterotrimer; immunoglobulin

Query Match
 Best Local Similarity 86.7%; Score 13; DB 2; Length 11;
 Pred. No. 8.1e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 |
 |
 Db 1 GTY 3

RESULT 4
 PT0214
 T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
 C/Accession: PT0214
 R/Nakano, N.; Kikuchi, H.; Nishimoto, H.; Kishimoto, T.
 J. Exp. Med. 173, 1091-1097, 1991
 A/Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted
 A/Reference number: PT0209; MUID:91217621; PMID:1902501
 A/Accession: PT0214
 A/Molecule type: mRNA
 A/Residues: 1-11 <NAK>
 C/Keywords: T-cell receptor

Query Match
 Best Local Similarity 86.7%; Score 13; DB 2; Length 11;
 Pred. No. 8.1e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 |
 |
 Db 5 GTY 7

RESULT 5
 A33099
 163K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
 C/Species: Plasmodium falciparum
 C/Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C/Accession: A33099
 R/Nichols, J.H.; Hager, L.P.
 submitted to the Protein Sequence Database, May 1990
 A/Reference number: A33098
 A/Accession: A33099
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-12 <NTC>

Query Match
 Best Local Similarity 86.7%; Score 13; DB 2; Length 12;
 Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 |
 |
 Db 9 GTY 11

RESULT 6
 S47391

T-cell antigen receptor VJ junction beta chain - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C/Accession: S47391; S47386
 R/Lehner, P.J.
 submitted to the EMBL Data Library, August 1994
 A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T
 A/Reference number: S47391
 A/Accession: S47391
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-12 <LEH>
 A/Cross-references: EMBL:Z35712; NID:G527519; PIDN:CAA84784.1; PID:G527520; EMBL:Z35701
 C/Keywords: T-cell receptor

Query Match
 Best Local Similarity 86.7%; Score 13; DB 2; Length 12;
 Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 |
 |
 Db 6 GSY 8

RESULT 7
 S47395
 T-cell antigen receptor VJ junction beta chain - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C/Accession: S47395
 R/Lehner, P.J.
 submitted to the EMBL Data Library, August 1994
 A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T
 A/Reference number: S47355
 A/Accession: S47395
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-12 <LEH>
 A/Cross-references: EMBL:Z35715; NID:G527525; PIDN:CAA84784.1; PID:G527526
 C/Keywords: T-cell receptor

Query Match
 Best Local Similarity 86.7%; Score 13; DB 2; Length 12;
 Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 |
 |
 Db 6 GSY 8

RESULT 8
 PH1611
 Ig H chain V-D-J region (wild-type clone 341) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1611
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
 A/Reference number: PH1580; MUID:93301609; PMID:8315387
 A/Accession: PH1611
 A/Molecule type: DNA
 A/Residues: 1-12 <LEV>
 A/Experimental source: bone marrow pre-B lymphocyte
 C/Keywords: immunoglobulin

Query Match
 Best Local Similarity 86.7%; Score 13; DB 2; Length 12;
 Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 |
 |
 Db 5 GSY 7

RESULT 9

PH0802
T-cell receptor alpha chain (M2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0802
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
J. Title: T cell receptor genes in a series of class I major histocompatibility complex-2 allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0802
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X60910
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 6 GTY 8

RESULT 10

PH0790
T-cell receptor alpha chain (OB7.3.2 V-alpha-4.3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0790
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
J. Title: T cell receptor genes in a series of class I major histocompatibility complex-2 allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0790
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X60895
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 6 GTY 8

RESULT 11

S47368
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47368
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T
A/Reference number: S47355
C/Accession: S47368
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:X35693; NID:9527477; PIDN:CAA84762.1; PID:9527478
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 7 GAY 9

RESULT 12

S47383
T-cell antigen receptor VI junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47383
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-R*0201 restricted recognition of influenza A is dominated by T
A/Reference number: S47355
C/Accession: S47383
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:X35709; NID:9527513; PIDN:CAA84778.1; PID:9527514
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 7 GSY 9

RESULT 13

PH0788
T-cell receptor alpha chain (B22 V-alpha-8.F3.4) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0788
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
J. Title: T cell receptor genes in a series of class I major histocompatibility complex-2 allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0788
A/Molecule type: mRNA
A/Residues: 1-13 <CAS>
A/Cross-references: EMBL:X60893
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 7 GTY 9

RESULT 14

PQ0700
unidentified 6.3/40K protein [imported] - rice (fragment)
C/Species: Oryza sativa (rice)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: PQ0700
R/Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
J. Title: A rice protein library; a data-file of rice proteins separated by two-dimensio
A/Reference number: PQ0696
A/Accession: PQ0700

A>Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-13 <KOM>
 A/Cross-references: UNIPROT:Q7M1U1

Query Match 86.7%; Score 13; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 9.5e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 |
 Db 3 GAY 5

RESULT 15

A59018

MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998

C/Accession: A59018

R/Abbe, M.; Smith, C.J.; Larson, C.U.

submitted to the Protein Sequence Database, May 1998

A/Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a bre

A/Reference number: A59018

A/Accession: A59018

A/Molecule type: protein

A/Residues: 1-14 <ABE>

A/Experimental source: breast cancer cell line MCF-7

A/Note: 3-Val was also found

C/Keywords: DNA binding; heterodimer

Query Match 86.7%; Score 13; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 |
 Db 6 GSY 8

Search completed: December 13, 2004, 22:32:58
 Job time : 16.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:00:41; Search time 83.8 seconds
(without alignments)
27.464 Million cell updates/sec

Title: US-10-068-905-5

Perfect score: 15

Sequence: 1 GXYX 4

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	86.7	8	1 UF06_MOUSE	P38644 mus muscula
2	13	86.7	9	2 Q9QWTO	Q9QWTO mus muscula
3	13	86.7	10	2 Q8NEY9	Q8NEY9 homo sapien
4	13	86.7	10	2 AA063472	AA063472 homo sapi
5	13	86.7	11	2 Q9UC46	Q9UC46 homo sapien
6	13	86.7	11	2 Q7YR62	Q7YR62 homo sapien
7	13	86.7	13	1 ADFB_TENMO	P82432 tenebrio mo
8	13	86.7	13	2 Q7YOR1	Q7YOR1 brassica ju
9	13	86.7	13	2 Q7YOR1	Q7YOR1 brassica ju
10	13	86.7	13	2 Q7YOR1	Q7YOR1 brassica ju
11	13	86.7	15	1 PH3_PRUSE	P29265 prunus sero
12	13	86.7	15	1 UCL1_MAIZE	P80620 zea mays (m
13	13	86.7	15	2 Q9S8T4	Q9S8T4 zea mays (m
14	13	86.7	15	2 Q47892	Q47892 fireyeella d
15	13	86.7	15	2 Q47893	Q47893 fireyeella d
16	13	86.7	16	1 PH2_PRUSE	P29264 prunus sero
17	13	86.7	16	2 Q7YOR1	Q7YOR1 brassica ju
18	13	86.7	16	2 Q6UDK5	Q6UDK5 canis fami
19	13	86.7	16	2 Q9SMW3	Q9SMW3 arabidopsis
20	13	86.7	17	2 Q6LC19	Q6LC19 homo sapien
21	13	86.7	17	2 Q6Z645	Q6Z645 saguinus oe
22	13	86.7	17	2 Q71VQ4	Q71VQ4 homo sapien
23	13	86.7	17	2 Q9T2H6	Q9T2H6 spinacia ol
24	13	86.7	17	2 Q84098	Q84098 influenza a
25	13	86.7	17	2 Q71ZNI	Q71ZNI torpedo mar
26	13	86.7	17	2 AAC39714	AAC39714 homo sapi
27	13	86.7	18	2 AAB92363	AAB92363 homo sapi
28	13	86.7	18	2 Q9GUM1	Q9GUM1 lagenorthinc
29	13	86.7	18	2 Q9GUM2	Q9GUM2 lagenorthinc
30	13	86.7	18	2 Q9GUM3	Q9GUM3 lagenorthinc
31	13	86.7	18	2 Q6LD78	Q6LD78 clostridium

32	13	86.7	18	2 Q9R4C6	Q9R4C6 agrobacteri
33	13	86.7	18	2 Q9R4F9	Q9R4F9 aeromonas.
34	13	86.7	18	2 Q9R501	Q9R501 bacillus su
35	13	86.7	18	2 Q9PRX1	Q9PRX1 struthio ca
36	13	86.7	18	2 AAB20893	AAB20893 clostridi
37	13	86.7	19	2 Q9N613	Q9N613 toxoplasma
38	13	86.7	19	2 Q9GNL6	Q9GNL6 dirosophila
39	13	86.7	19	2 Q47895	Q47895 fireyeella d
40	13	86.7	19	2 Q9R4F8	Q9R4F8 aeromonas.
41	13	86.7	19	2 Q9R6J8	Q9R6J8 yersinia pe
42	13	86.7	20	1 PYRR_PRRAP	PYRR_PRRAP pyrrhocoris
43	13	86.7	20	2 Q25281	Q25281 leishmania
44	13	86.7	20	2 Q9GNL7	Q9GNL7 dirosophila
45	13	86.7	20	2 Q9S8H8	Q9S8H8 brassica na

ALIGNMENTS

RESULT 1
ID UF06_MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Seikirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.2, its MW is: 50 kDa.
KW Direct protein sequencing.
FT NON TER
SQ SEQUENCE 8 AA; 817 MW; A35DD87676B05B1 CRC64;

Query Match Score 13; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. NO. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 6 GAY 8

RESULT 2
ID Q9QWTO PRELIMINARY; PRT; 9 AA.
AC Q9QWTO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 13, Last annotation update)
DE Proteinase 3 (Myeloblastic) (Fragment).
GN Name=Prtn3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SV129 D3;
RA Lutz P.G., Moeg-Lutz C., Houzel-Charavel A., Cayre Y.E.;
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL, AJ007030; CAA07423.1; -.

DR MGD_MGI:893580; Prit3.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 937 MW; C91E75A77B45B87D CRC64;

Query Match 86.7%; Score 13; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 3 GSY 5

RESULT 3

Q8NE9 PRELIMINARY; PRT; 10 AA.
 AC Q8NE9; 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Type II hair-specific keratin (Type II hair keratin) (Fragment).
 GN Name-KRT86;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Baitwa N.K., Bamezai R.;
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Baitwa N.K., Bamezai R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY037552; AA68688.1; -;
 DR EMBL; AY203963; AA063472.1; -;
 DR GO; GO:0005882; C:intermediate filament; IEA.
 KW Keratin.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1034 MW; 9B53417EAB45B87E CRC64;

Query Match 86.7%; Score 13; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6.6e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 4 GSY 6

RESULT 4

AA063472 PRELIMINARY; PRT; 10 AA.
 AC AA063472; 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Type II hair keratin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Baitwa N.K., Bamezai R.;
 RL "Study of promoter polymorphism of type II hair keratin gene hnb6";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY203963; AA063472.1; -;
 KW Keratin.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1034 MW; 9B53417EAB45B87E CRC64;

Query Match 86.7%; Score 13; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 6.6e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 4 GSY 6

RESULT 5

Q9UC46 PRELIMINARY; PRT; 11 AA.
 AC Q9UC46; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Neutrophil inhibitor peptide, NIP=POLYMORPHONUCLEAR neutrophil inhibitor peptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96326114; PubMed=8703476;
 RA Cooper J.A., Jr.; Culbreth R.R.;
 RT "Characterization of a neutrophil inhibitor peptide harvested from human bronchial lavage: homology to influenza A nucleoprotein";
 RL Am. J. Respir. Cell Mol. Biol. 15:207-215 (1996).
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0030236; P:anti-inflammatory response; NAS.
 SQ SEQUENCE 11 AA; 1262 MW; 951A1C3279C9DB45 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 7.2e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 3 GSY 5

RESULT 6

Q7YP62 PRELIMINARY; PRT; 11 AA.
 AC Q7YP62; 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE MHC class IB antigen (Fragment).
 GN Name-HLA-F;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Y., He X., Xu L., Zeng Y.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY28516; AAP94210.1; -;
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1208 MW; 2E0B6C5C05AB5B8 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 7.2e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 4 GSY 6

RESULT 7

ADPB_TENMO

ID ADBF_TEMPO STANDARD; PRT; 13 AA.
AC P83109;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antidiuretic factor B (ADFB)
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
RP SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=22465067; PubMed=12576082;
RA Elgenheer R.A., Wihart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,
Hull U.J., Schooley D.A.;
RT "Isolation, identification and localization of a second beetle
antidiuretic peptide."
RT antidiuretic peptide."
RU Peptides 24:27-34(2003).
CC -1- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses
CC GMP as second messenger. May function as an antidiuretic hormone.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two
CC pairs of bilaterally symmetrical cells in the protocerebrum.
CC -1- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI; RANGE=1-13;
CC NOE=Ref.1.
KW Direct protein sequencing; Hormone; Neuropeptide.
SQ SEQUENCE 13 AA; 1562 MW; 02404504B8A632B CRC64;

Query Match 86.7%; Score 13; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
DB 4 GSY 6

RESULT 8
P82432 PRELIMINARY; PRT; 13 AA.
AC P82432;
DT 01-JUN-2000 (TRENBLrel. 14, Created)
DT 01-JUN-2000 (TRENBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE 32 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PERIT HAYANA.
RA Bies K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture."
RU Planta 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1307 MW; D5022297D8697DC6 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3

DB 9 GAY 11

RESULT 9
O7MUT1 PRELIMINARY; PRT; 13 AA.
AC O7MUT1;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Unidentified 6.3/40K protein (Fragment).
OS Oryza sativa (rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA Komatsu S., Kajiwara H., Hirano H.;
RT "A rice protein library: a data-file of rice proteins separated by
RT two-dimensional electrophoresis."
RU Theor. Appl. Genet. 86:935-942(1993).
DR PIR; PQ0700; PQ0700.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1218 MW; 27BA7291E7D3D878 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
DB 3 GAY 5

RESULT 10
O7YOR1 PRELIMINARY; PRT; 13 AA.
AC O7YOR1;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 25, Last annotation update)
DE Gamma-glutamylcysteine synthetase (EC 6.3.2.2) (Fragment).
GN Name=gsu1;
OS Brassica juncea (leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eurosid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RP SEQUENCE FROM N.A.
RA Wächter A., Steinger H., Rausch T., Bogs J.;
RU Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564376; CAD91995.1; -;
DR GO; GO:0004357; F:glutamate-cysteine ligase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
KW Ligase.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1266 MW; DBF2097182417DC6 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
DB 9 GAY 11

RESULT 11
PH3_PROSE

ID PH3_PRUSE STANDARD; PRT; 15 AA.
 AC P29265;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Prunasin beta-glucosidase IIB (EC 3.2.1.118) (Prunasin hydrolase
 isozyme IIB) (P11B) (Fragment).
 OS Prunus serotina (Black cherry).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 NCBI_TaxID=23207;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Seed;
 RA Li C.P., Swain E., Poulton J.E.;
 RL "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
 RL Plant Physiol. 100:282-290(1992).
 CC -1- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-
 CC glucose.
 CC -1- SUBUNIT: Monomer.
 CC -1- DEVELOPMENTAL STAGE: Absent from maturing black cherry fruits
 CC until 6 weeks after flowering. Then, concomitant with cotyledon
 CC development, the level of enzyme increases with specificity for
 CC embryonal tissues.
 CC -1- PTM: Glycosylated.
 CC -1- PTM: Glycosylated.
 KW Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
 KM Multigene family.
 PT NON_TER
 PT 15
 SQ SEQUENCE 15 AA; 1635 MW; 4E3D7F4F990CFE4C CRC64;

Query Match 86.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 1 GY 3

RESULT 12
 UC14_MAIZE STANDARD; PRT; 15 AA.
 ID UC14_MAIZE
 AC P80620;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 258)
 DE (fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RT Pernotier J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.9, its MW is: 34.6 kDa.
 DR Maize-2DPAGE; P80620; COLEOPTILE.
 DR MaizeDB; 123944;
 KW Direct protein sequencing.
 FT NON_TER
 FT 15
 SQ SEQUENCE 15 AA; 1564 MW; CFOBBA0B7DE658 CRC64;

Query Match 86.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 DB 7 GAY 9

RESULT 13
 Q9S8L4 PRELIMINARY; PRT; 15 AA.
 ID Q9S8L4
 AC Q9S8L4;
 DT 01-MAY-2000 (TRENBERG. 13, Created)
 DT 01-MAY-2000 (TRENBERG. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBERG. 24, Last annotation update)
 DE Beta-D-glucoside glucosylase (EC 3.2.1.21) (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94347094; Pubmed=8068000;
 RA Feldwisch J., Vente A., Zetel R., Bako L., Campos N., Palme K.;
 RT "Characterization of two membrane-associated beta-glucosidases from
 RT maize (Zea mays L.) coleoptiles."
 RL Biochem. J. 302:15-21(1994).
 DR GO:0008442; F:beta-glucosidase activity; IEA.
 SQ SEQUENCE 15 AA; 1667 MW; 46C40370DC8C730B CRC64;

Query Match 86.7%; Score 13; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 3 GSY 5

RESULT 14
 Q47892 PRELIMINARY; PRT; 15 AA.
 ID Q47892
 AC Q47892;
 DT 01-NOV-1996 (TRENBERG. 01, Created)
 DT 01-NOV-1996 (TRENBERG. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBERG. 24, Last annotation update)
 DE Beta-allophycocyanin (fragment).
 OS Fremyella diplosiphon (Calothrix PCC 7601).
 OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
 NCBI_TaxID=1197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86233345; Pubmed=3086870;
 RA Conley P.B., Lemaux P.G., Lomax T.L., Grossman A.R.;
 RT "Genes encoding major light harvesting polypeptides are clustered on
 RT the genome of the cyanobacterium Fremyella diplosiphon."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928(1986).
 DR EMBL; M13216; AAA24871.1;
 FT NON_TER
 FT 1
 SQ SEQUENCE 15 AA; 1644 MW; 97271656699F62F CRC64;

Query Match 86.7%; Score 13; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 4 GSY 6

RESULT 15
 Q47893 PRELIMINARY; PRT; 15 AA.

Tue Dec 14 10:04:27 2004

us-10-068-905-5.rup

Page 5

AC Q47893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 08, last annotation update)
DE Beta-phycocyanin (Fragment).
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
OX NCBI_TaxId=1197;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86233345; PubMed=3086870;
RA Conley P.B., Lemaux P.G., Lomax T.L., Grossman A.R.;
RT "Genes encoding major light-harvesting polypeptides are clustered on
the genome of the cyanobacterium Fremyella diplosiphon.",
RL Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928 (1986).
DR EMBL, M13217; AAA24880.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1528 MW; 7FF2F65518F493D4 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 4 GSY 6

Search completed: December 13, 2004, 22:31:36
Job time : 85.8 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 21:59:41 ; Search time 80 Seconds
(without alignments)
17.936 Million cell updates/sec

Title: US-10-068-905-6

Perfect score: 15

Sequence: 1 GXYY 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	13	86.7	4 1 AAP61656	Aap61656 Sequence
2	13	86.7	4 1 AAP71313	Aap71313 Peptide c
3	13	86.7	4 2 AAR55333	Aar55333 Inhibitor
4	13	86.7	4 2 AAR75499	Aar75499 Csa recep
5	13	86.7	4 5 ABP55713	Abp55713 B15 class
6	13	86.7	4 5 ABP55796	Abp55796 B15 class
7	13	86.7	4 5 ABG96845	Abg96845 Human leu
8	13	86.7	4 5 ABG97024	Abg97024 Human leu
9	13	86.7	4 5 ABG96697	Abg96697 Human leu
10	13	86.7	4 5 ABP67652	Abp67652 Human CD6
11	13	86.7	4 5 ABP67653	Abp67653 Human CD6
12	13	86.7	4 5 AAR84247	Aar84247 Caspase c
13	13	86.7	4 6 ABJ18638	Abj18638 ExDB rece
14	13	86.7	4 6 ABP59243	Abp59243 Peptide e
15	13	86.7	4 7 ADJ81984	Adj81984 Thermus b
16	13	86.7	4 7 ADL98858	Adl98858 Human leu
17	13	86.7	4 7 ADL98369	Adl98369 Human leu
18	13	86.7	4 7 ADL98514	Adl98514 Human leu
19	13	86.7	4 7 ADL98678	Adl98678 Human leu
20	13	86.7	4 8 ADK42069	Adk42069 Antibacte
21	13	86.7	4 8 ADK42068	Adk42068 Antibacte
22	13	86.7	5 2 AAR43432	Aar43432 Rc/SSA ep
23	13	86.7	5 2 AAR56301	Aar56301 Second ge
24	13	86.7	5 2 AAR56298	Aar56298 Synthetic
25	13	86.7	5 2 AAR72555	Aar72555 Pertussis

26	13	86.7	5 2 AAR72549	Aar72549 Pertussis
27	13	86.7	5 2 AAR72699	Aar72699 Kappa-cas
28	13	86.7	5 2 AAY41820	Aay41820 Pertussis
29	13	86.7	5 2 AAY41826	Aay41826 Pertussis
30	13	86.7	5 2 AAW95230	AAW95230 PT toxin
31	13	86.7	5 2 AAW95236	AAW95236 PT toxin
32	13	86.7	5 2 AAY43373	Aay43373 Pertussis
33	13	86.7	5 2 AAY43367	Aay43367 Pertussis
34	13	86.7	5 3 AAY44679	Aay44679 Hydropero
35	13	86.7	5 3 AAY68369	Aay68369 Pertussis
36	13	86.7	5 3 AAY68375	Aay68375 Pertussis
37	13	86.7	5 3 AAB08397	Aab08397 Peptide d
38	13	86.7	5 4 AAB66243	Aab66243 B pertuss
39	13	86.7	5 4 AAB66249	Aab66249 B pertuss
40	13	86.7	5 5 ABP67641	Abp67641 Human CD6
41	13	86.7	5 5 ABP67642	Abp67642 Human CD6
42	13	86.7	5 5 AAE16333	AAE16333 N-termi
43	13	86.7	5 5 AAB75621	Abb75621 Anti-RANK
44	13	86.7	5 6 ABJ18639	Abj18639 ErbB rece
45	13	86.7	5 6 ABP59244	Abp59244 Peptide e

ALIGNMENTS

RESULT 1	
ID AAP61656	standard; protein; 4 AA.
XX	
AC AAP61656;	
XX	
AC	
XX	
DT 25-MAR-2003	(revised)
DT 03-OCT-2002	(revised)
DT 21-AUG-1991	(first entry)
XX	
DE	
DE	Sequence of peptide which inhibits cyclic-nucleotide independent protein
DE	kinase activity and mammalian cell growth.
XX	
KW	Cell growth inhibitor; tumour cell growth inhibitor.
XX	
OS	Synthetic.
XX	
FH	
FT	Key Location/Qualifiers
FT	Misc-difference 1 /label= Carbobenzoxy-Phe
FT	Misc-difference 4 /label= Tyr-CH2Cl
XX	
PN	US4582821-A.
XX	
PD	15-APR-1986.
XX	
PF	16-NOV-1983; 83US-00552255.
XX	
PR	16-NOV-1983; 83US-00552255.
XX	
PA	(DUPO) DU POINT DE MEMOIRS & CO E I.
XX	
PI	Kettner CA; Racker E;
XX	
DR	WPI; 1986-118872/18.
XX	
PT	Inhibition of tumour cell growth - using peptide and aminoacid
XX	halo:methyl ketone(s).
XX	
PS	Claim 1; Col 4; 9pp; English.
XX	
CC	The cpds. of the invention inhibit protein phosphorylation. The inventors
CC	claim a process for inhibiting the growth of tumour cells in a medium
CC	which comprises contacting the cells with a cpd. of formula (AAP61654-
CC	P61661) or a physiologically acceptable salt. (Updated on 03-OCT-2002 to
CC	add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX	

SQ Sequence 4 AA;
 Query Match 86.7%; Score 13; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 1 1
 2 GAY 4

Db 2 GAY 4

RESULT 2
 AAR71313
 ID AAR71313 standard; protein; 4 AA.
 XX
 XX AAR71313;
 AC
 XX 25-MAR-2003 (revised)
 DT 15-MAY-1991 (first entry)
 XX
 XX Peptide component of cpd. for treating picornavirus infections.
 DE
 XX Picornaviridae; poliovirus; rhinovirus; antiviral agent.
 XX
 XX Synthetic.
 OS
 XX US4636492-A.
 PN
 XX 13-JAN-1987.
 PD
 XX 29-AUG-1984; 84US-00645426.
 PF
 XX 29-AUG-1984; 84US-00645426.
 PR
 XX (DUPO) DU FONT DE NEMOURS & CO E I.
 PA
 XX Ketner CA, Korant BD;
 PI
 XX WPI; 1987-036897/05.
 DR
 XX Treating picorna-virus infection with peptide halo:methyl ketone cpds. -
 PT esp. for treating polio virus and rhino virus infections.
 XX
 XX Disclosure; Page 4; 10pp; English.
 PS
 XX This peptide is useful as part of a peptide/halo-methyl ketone cpd., for
 CC treating picornavirus, espilo- or rhinovirus infections. It inhibits the
 CC processing of picornavirus capsid proteins by virus encoded proteases.
 CC See AAR71301-12. See also US4652552. (Updated on 25-MAR-2003 to correct
 CC PA field.)
 CC
 SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 1 1
 2 GAY 4

Db 2 GAY 4

RESULT 3
 AAR55333
 ID AAR55333 standard; peptide; 4 AA.
 XX
 XX AAR55333;
 AC
 XX 25-MAR-2003 (revised)
 DT 30-JAN-1995 (first entry)
 XX
 XX Inhibitor of tyrosine kinase.
 DE
 XX

KW PTK; signal transduction; proliferation; cancer; psoriasis; viral;
 KM inflammatory; allergic; cardiovascular; diseases.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FT Modified-site 3 /note="Tyr(2,3,5,6-P4) (D/L)"
 FT
 FT
 FN MO9411392-A1.
 PN
 XX 26-MAY-1994.
 PD
 XX 03-NOV-1993; 93WO-US010610.
 PF
 XX 06-NOV-1992; 92US-00973136.
 PR 27-OCT-1993; 93US-00139913.
 XX
 XX (WARN) WARNER LAMBERT CO.
 PA
 XX Dobrusin EM, Mcnamara DJ, Fry DW, Singh J;
 PI
 XX WPI; 1994-183419/22.
 DR
 XX New peptide inhibitors of protein tyrosine kinase - contain D-Tyr or
 PT tetrafluoro-Tyr residue, for treating proliferative diseases, viral
 PT infection, inflammation etc.
 XX
 XX Claim 7; Page 36; 44pp; English.
 PS
 XX The sequence is that of a protein tyrosine kinase inhibitor conrg. D- Tyr
 CC or tetrafluoro-Tyr residues. The peptide can be used to inhibit TK-
 CC mediated signal transduction and is useful for controlling proliferative
 CC diseases, e.g. cancer, psoriasis and to treat viral, inflammatory,
 CC allergic and cardiovascular diseases. See also AAR55302-39. (Updated on
 CC 25-MAR-2003 to correct FN field.)
 CC
 SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 1 1
 1 GAY 3

Db 1 GAY 3

RESULT 4
 AAR75499
 ID AAR75499 standard; peptide; 4 AA.
 XX
 XX AAR75499;
 AC
 XX 25-MAR-2003 (revised)
 DT 13-NOV-1995 (first entry)
 XX
 XX C5a receptor-antagonist core tetrapeptide.
 DE
 XX C5a; C5a receptor-antagonist; antiinflammatory.
 KM
 XX Homo sapiens.
 XX
 XX MO9516033-A1.
 PN
 XX 15-JUN-1995.
 PD
 XX 16-NOV-1994; 94WO-IB000359.
 PF
 XX 06-DEC-1993; 93US-00162591.
 PR
 XX (CIBA) CIBA GEIGY AG.
 PA
 XX

PI Van Oostrum J, Boyar WC, Galakatos NG, Reppard JV;
 XX WPI; 1995-224319/29.
 DR
 XX C5a receptor antagonists having no agonist activity - are used in
 PT compns. to treat C5a-mediated diseases and inflammatory conditions.
 XX
 XX Disclousre; Page 36; 65pp; English.
 PS
 CC Polypeptide receptor antagonists to C5a contain an essential core
 CC tetrapeptide (AAK75498 or AAK75499) or core tripeptide (DGA) which
 CC displays C5a blocking activity. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 4 AA;

Query Match 86.7%; Score 13; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 1
 2 GAY 4

RESULT 5
 ABP55713
 ID ABP55713 standard; peptide; 4 AA.

AC ABP55713;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE B15 class I sHLA molecule ligand related peptide #7.

XX HLA ligand; human leukocyte antigen; predictive algorithm; database;
 KM MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
 XX
 OS Synthetic.

PN WO200269198-A2.

PD 06-SEP-2002.

PF 21-FEB-2002; 2002WO-US005298.

PR 21-FEB-2001; 2001US-0270357P.
 PR 10-OCT-2001; 2001US-00974366.
 PR 18-DEC-2001; 2001US-00022066.

PA (HILD/) HILDEBRAND W H.
 PA (PRIL/) PRILLIMAN K R.
 PA (HICK/) HICKMAN H D.

PI Hildebrand WH, Prilliman KR, Hickman HD;
 XX WPI; 2002-732755/79.

PT Human leukocyte antigen ligand database assembled by producing HLA having
 PT loaded ligands, isolating and sequencing loaded ligands to obtain HLA
 PT ligand data and populating database in computer system with ligand data.

XX Disclousre; Fig 5; 118pp; English.

XX The present invention describes a human leukocyte antigen (HLA) (e.g.
 CC soluble HLA) ligand database assembled by a process which involves
 CC providing a computer system capable of storing HLA data as a database,
 CC producing HLA having ligands loaded on it, isolating the loaded ligands
 CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
 CC populating the database with HLA ligand data. Also described: (1)
 CC accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
 CC system for HLA (e.g. sHLA) ligand database. The database is populated
 CC with HLA ligand sequences, motifs, extended motifs, submotifs, ligands

CC unique to infected cells, tumour specific ligands, as well as a
 CC collection of current and future developed HLA ligand sequences. The
 CC database which contains endogenously bound and loaded ligands facilitates
 CC searching of viral, bacterial, tumour or human protein sequences for
 CC ligands likely to bind a particular HLA class I or class II protein. The
 CC database allows the user to screen an unknown peptide sequence for
 CC potential matches with sHLA ligand discrete sequences or sHLA ligand
 CC motifs of sequences. Due to the completeness and concentration of sHLA
 CC obtained to date, better sequencing data of numerous endogenously loaded
 CC HLA ligands is found in the sHLA ligand database, and by comparison of
 CC such ligands to each other and to the genomic sequence, better motifs are
 CC also found in the sHLA ligand database. ABP55692 to ABP5512 represent
 CC amino acid sequences used in the exemplification of the present invention
 XX

XX Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 1
 2 GAY 4

RESULT 6
 ABP55796
 ID ABP55796 standard; peptide; 4 AA.

AC ABP55796;
 XX
 DT 25-FEB-2003 (first entry)
 XX

DE B15 class I sHLA molecule ligand related peptide #90.

XX HLA ligand; human leukocyte antigen; predictive algorithm; database;
 KM MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
 XX
 OS Synthetic.

PN WO200269198-A2.

PD 06-SEP-2002.

PF 21-FEB-2002; 2002WO-US005298.

PR 21-FEB-2001; 2001US-0270357P.
 PR 10-OCT-2001; 2001US-00974366.
 PR 18-DEC-2001; 2001US-00022066.

PA (HILD/) HILDEBRAND W H.
 PA (PRIL/) PRILLIMAN K R.
 PA (HICK/) HICKMAN H D.

PI Hildebrand WH, Prilliman KR, Hickman HD;
 XX WPI; 2002-732755/79.

PT Human leukocyte antigen ligand database assembled by producing HLA having
 PT loaded ligands, isolating and sequencing loaded ligands to obtain HLA
 PT ligand data and populating database in computer system with ligand data.

XX Disclousre; Fig 5; 118pp; English.

XX The present invention describes a human leukocyte antigen (HLA) (e.g.
 CC soluble HLA) ligand database assembled by a process which involves
 CC providing a computer system capable of storing HLA data as a database,
 CC producing HLA having ligands loaded on it, isolating the loaded ligands
 CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
 CC populating the database with HLA ligand data. Also described: (1)
 CC accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
 CC system for HLA (e.g. sHLA) ligand database. The database is populated
 CC with HLA ligand sequences, motifs, extended motifs, submotifs, ligands

CC unique to infected cells, tumour specific ligands, as well as a
CC collection of current and future developed HLA ligand sequences. The
CC database which contains endogenously bound and loaded ligands facilitates
CC searching of viral, bacterial, tumour or human protein sequences for
CC ligands likely to bind a particular HLA class I or class II protein. The
CC database allows the user to screen an unknown peptide sequence for
CC potential matches with SHLA ligand discrete sequences or SHLA ligand
CC motifs of sequences. Due to the completeness and concentration of SHLA
CC obtained to date, better sequencing data of numerous endogenously loaded
CC HLA ligands is found in the SHLA ligand database, and by comparison of
CC such ligands to each other and to the genomic sequence, better motifs are
CC also found in the SHLA ligand database. ABP55692 to ABP55912 represent
CC amino acid sequences used in the exemplification of the present invention
SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GAY 4

RESULT 7
ABG96845
ID ABG96845 standard; peptide; 4 AA.
XX
AC ABG96845;
XX

DT 16-DEC-2002 (first entry)

DE Human leukocyte antigen (HLA) B15 ligand #170.

XX Soluble human leukocyte antigen; HLA; SHLA; cell pharm;
XX multicentric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
XX viral infection; cancer; autoimmune disease; vaccine development; MHC;
XX major histocompatibility complex; diagnostic development;
XX HLA class I polymorphism; HLA-B15 allotype; ligand.

OS Homo sapiens.

XX MO200262846-A2.

PD 15-AUG-2002.

PF 18-DEC-2001; 2001WO-US049744.

PR 18-DEC-2000; 2000US-0256409P.

PR 18-DEC-2000; 2000US-0256410P.

PR 10-OCT-2001; 2001US-00974366.

XX (HIL/D/) HILDEBRAND W H.

XX (PRIL/) PRILLIMAN K R.

PI Hildebrand WH, Prilliman KR;

DR WPI; 2002-698563/75.

XX Producing soluble human leukocyte antigen (HLA) in cell pharm useful for

PT studies of peptide loading for characterizing human immune responses

PT involves using HLA allelic cDNA or genomic DNA as starting material.

XX Disclosure; Page 178; 300pp; English.

XX The invention describes a method of producing soluble human leukocyte

CC antigen (HLA) molecules (SHLA) in cell pharm involving amplifying HLA

CC allelic DNA by PCR using a locus specific primer to produce truncated a

CC PCR product (PI), inserting PI into mammalian expression vector;

CC electroporating the plasmid into a host cell; inoculating the cell pharm

CC with the host cell such that cell pharm produces SHLA. A multicentric HLA

CC complex (I) is useful for testing functionality of peptide ligands bound

CC by at least two soluble HLA molecules. (I) can be tested for its ability
CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
CC responses in humans. (I) is useful for studying T cell responses to
CC pathological conditions such as viral infections and cancer, and for
CC modulating the human immune system to induce tolerance in autoimmune
CC diseases. The individual secreted major histocompatibility complex (MHC)
CC molecules produced are useful for studies of peptide loading (i.e., in
CC vaccine development) and to the development of diagnostics. With the
CC secreted MHC molecules, naturally loaded peptides can be eluted from the
CC MHC molecule and characterised. The secreted MHC molecules allow the
CC assessment of structural and functional impact of HLA class I
CC polymorphism. The molecules are also useful to generate ligands and hence
CC ligand maps from the peptide pools extracted from series of distinct yet
CC related class I HLA-B15 allotypes; compare the different ligand maps to
CC identify potentially shared elements; and characterise the elements
CC identified to positively or negatively validate the occurrence of
CC overlapping ligands. The truncated version of (MHC) can be produced in
CC mammalian or insect/bacterial cells such that milligram or greater
CC quantities of an individual class I or class II molecule can be obtained.
CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
XX

SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GAY 4

RESULT 8
ABG97024
ID ABG97024 standard; peptide; 4 AA.
XX

AC ABG97024;

DT 16-DEC-2002 (first entry)

DE Human leukocyte antigen (HLA) B15 ligand #352.

XX Soluble human leukocyte antigen; HLA; SHLA; cell pharm;
XX multicentric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
XX viral infection; cancer; autoimmune disease; vaccine development; MHC;
XX major histocompatibility complex; diagnostic development;
XX HLA class I polymorphism; HLA-B15 allotype; ligand.

OS Homo sapiens.

XX MO200262846-A2.

PD 15-AUG-2002.

PF 18-DEC-2001; 2001WO-US049744.

PR 18-DEC-2000; 2000US-0256409P.

PR 18-DEC-2000; 2000US-0256410P.

PR 10-OCT-2001; 2001US-00974366.

XX (HIL/D/) HILDEBRAND W H.

XX (PRIL/) PRILLIMAN K R.

PI Hildebrand WH, Prilliman KR;

DR WPI; 2002-698563/75.

XX Producing soluble human leukocyte antigen (HLA) in cell pharm useful for

PT studies of peptide loading for characterizing human immune responses

PT involves using HLA allelic cDNA or genomic DNA as starting material.

XX Disclosure; Page 183; 300pp; English.

The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA allelic DNA by PCR using a locus specific primer to produce truncated PCR product (PI), inserting PI into mammalian expression vector, electroporating the plasmid into a host cell, inoculating the cell pharm with the host cell such that cell pharm produces sHLA. A multimeric HLA complex (I) is useful for testing functionality of peptide ligands bound by at least two soluble HLA molecules. (I) can be tested for its ability to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune responses in humans. (I) is useful for studying T cell responses to pathological conditions such as viral infections and cancer, and for modulating the human immune system to induce tolerance in autoimmune diseases. The individual secreted major histocompatibility complex (MHC) molecules produced are useful for studies of peptide loading (i.e., in vaccine development) and to the development of diagnostics. With the secreted MHC molecules, naturally loaded peptides can be eluted from the MHC molecule and characterised. The secreted MHC molecules allow the assessment of structural and functional impact of HLA class I polymorphism. The molecules are also useful to generate ligands and ligand maps from the peptide pools extracted from series of distinct yet related class I HLA-B*5 alleles, compare the different ligand maps to identify potentially shared elements; and characterise the elements identified to positively or negatively validate the occurrence of overlapping ligands. The truncated version of (MHC) can be produced in mammalian or insect/bacterial cells such that milligram or greater quantities of an individual class I or class II molecule can be obtained. This sequence represents a HLA (human leukocyte antigen) peptide ligand

```

Query Match      86.7%      Score 13; DB 5; Length 4;
Best Local Similarity 66.7%      Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 GAY 3
      2 GAY 4
Db

```

```

RESULT 9
ABG96697
ID      ABG96697  standard; peptide; 4 AA
vv

```

DT 16-DEC-2002 (first entry)
xx

Human leukocyte antigen (HLA) B15 ligand #120.

KM	Solidine human leukocyte antigen; HLA; SHLA; cell pham;
KM	multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response
KM	viral infection; cancer; autoimmune disease; vaccine development; MHC
KM	major histocompatibility complex; diagnostic development;
HLA class I polymorphism; HLA-B*5 alleotype; ligand.	

OS Homo sapiens.

PN WO200262846-A2

PD 15-AUG-2002.

18-DEC-2001; 2001WO-US049744

PR 18-DEC-2000; 2000US-0256409P

PR 10-OCT-2001; 2001US-00974366
yy

PA (HILD/) HILDEBRAND W H
DA (PRTI/) PRTITMAN Y D

XX HIJ d'abhandl WH D'ij 11:11

XX DB WPT: 2002-698563/75

DR WPI; 2002-698563/75.

XX Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
 XX studies of peptide loading for characterizing human immune responses
 XX involves using HLA allelic cDNA or genomic DNA as starting material.
 XX

Disclosure; Fig 26; 300pp; English.

The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules (SHLA) in cell pham involving amplifying HLA allelic DNA by PCR using a locus specific primer to produce truncated a PCR product (P1), inserting P1 into mammalian expression vector; electroporating the plasmid into a host cell; inoculating the cell pham with the host cell such that cell pham produces SHLA. A multimeric HLA complex (I) is useful for testing functionality of peptide ligands bound by at least two soluble HLA molecules. (I) can be tested for its ability to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune responses in humans. (I) is useful for studying T cell responses to pathological conditions such as viral infections and cancer, and for modulating the human immune system to induce tolerance in autoimmune diseases. The individual secreted major histocompatibility complex (MHC) molecules produced are useful for studies of peptide loading (i.e., in vaccine development) and to the development of diagnostics. With the secreted MHC molecules, naturally loaded peptides can be eluted from the MHC molecule and characterised. The secreted MHC molecules allow the assessment of structural and functional impact of HLA class I polymorphism. The molecules are also useful to generate ligands and ligand maps from the peptide pools extracted from series of distinct yet related class I HLA-B*55 alleles; compare the different ligand maps to identify potentially shared elements; and characterise the elements identified to positively or negatively validate the occurrence of overlapping ligands. The truncated version of (MHC) can be produced in mammalian or insect/bacterial cells such that milligram or greater quantities of an individual class I or class II molecule can be obtained. This sequence represents a HLA (human leukocyte antigen) peptide ligand

Query Match	86.7%;	Score 13;	DB 5;	Length 4;
Best Local Similarity	66.7%;	Pred. No. 1.7e+06;		
Matches	2;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0

QY 1 GXY 3
2 GAY 4

ID	ABP67652	standard; peptide; 4 AA.
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
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92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

DT 10-DEC-2002 (first entry)
 XX

Human CD66 family modulating peptide SEQ ID NO 523.

KM	Human; C66; CEACAM; cytostatic; antiinflammatory; immunomodulator; antibacterial; antiviral; gene therapy; vaccine; neutrophil;
KM	immune system; autoimmune disease; cancer; infection; bacterial; virus
KM	inflammatory disease; transplantation; immunisation.

Homo sapiens.

PN WO200268601-A2.
xx

PD 06-SEP-2002.

PF 27-FEB-2002; 2002WO-US005720
VV

PR 28-FEB-2001; 2001US-0272113P
YY

PA (SKUB/) SKUBITZ K M.
PA (SKUB/) SKUBITZ A P N

CC prevention or treatment of apoptosis-associated diseases, for the
 CC manufacture of a pharmaceutical agent and for identifying apoptosis
 CC modulators. The proteome is useful as a target for the diagnosis,
 CC prevention or treatment of apoptosis-associated diseases, and in a method
 CC for identifying apoptosis modulators. (1) is useful for treatment of
 CC hyperproliferative or degenerative diseases including cancers, autoimmune
 CC diseases, Alzheimer's disease, viral infections such as acquired
 CC immunodeficiency syndrome (AIDS) and vascular diseases such as myocardial
 CC infarction. (1) is also useful for treating and/or preventing diseases
 CC related to oxidative stress like ischemic stroke, arthritis, heart
 CC failure, Parkinson's disease and amyotrophic lateral sclerosis. (1) is
 CC also useful for develop modification-specific diagnostic tools. (1) is
 CC also useful for developing protein chips or other solid phase screening
 CC devices for high throughput screens, and also as a diagnostic tool to
 CC screen for caspase activity, and/or to determine the effectivity of
 CC caspase cleavage inhibiting and/or modulating substances. AAU84237-
 CC AAU84260 represent caspase cleavage sites of the invention
 XX

SO Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 1 GSY 3

RESULT 13
 ABJ18638
 ID ABJ18638 standard; peptide; 4 AA.
 XX
 AC ABJ18638;
 XX
 DT 20-FEB-2003 (first entry)
 XX
 DE ErbB receptor antagonist peptide #21.
 XX
 KM Vaccine; erbB receptor antagonist; tumour; cancer; gastric cancer;
 XX breast cancer; prostate cancer.
 XX
 OS Unidentified.
 XX
 PN WO200281649-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 08-APR-2002; 2002WO-US011211.
 XX
 PR 06-APR-2001; 2001US-0282937P.
 XX
 PR 03-AUG-2001; 2001US-0309864P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Greene MI, Zhang H, Murali R, Richter M, Berenzov A, Liu Q;
 PI Chen J;
 XX
 DR WPI; 2003-075482/07.
 XX
 PT New peptide antagonists against erbB receptors, useful for preventing or
 PT treating tumors or cancers (e.g. lung adenocarcinomas, breast carcinomas
 PT or prostate cancer) in humans.
 XX
 PS Claim 1; Page 82; 115pp; English.
 XX
 CC The invention comprises peptide antagonists designed to target erbB
 CC receptors. The erbB receptor peptide antagonists are useful for
 CC preventing tumors and cancers (e.g. gastric cancer, breast cancer and
 CC prostate cancer). The present amino acid sequence represents an erbB
 CC receptor peptide antagonist of the invention
 XX
 SO Sequence 4 AA;

Query Match 86.7%; Score 13; DB 6; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 2 GSY 4

RESULT 14
 ABP59243
 ID ABP59243 standard; peptide; 4 AA.
 XX

AC ABP59243;
 XX
 DT 10-MAY-2003 (first entry)
 XX

DE Peptide epitope for generating cell surface receptor antibody, SEQ ID 21.

XX Antibody; cytostatic; vaccine; cell surface receptor; erbB; TNF;
 XX immunoglobulin gene superfamily; IgSF; epitope.

XX Synthetic.

XX WO2003012072-A2.
 XX

PD 13-FEB-2003.
 XX

PF 05-AUG-2002; 2002WO-US024892.
 XX

PR 03-AUG-2001; 2001US-0309864P.
 XX

PA (UYPE-) UNIV PENNSYLVANIA.
 XX

PI Greene MI, Zhang H, Richter M, Murali R;
 PI WPI; 2003-268117/26.
 XX

PT Novel antibody for preventing, treating, imaging or diagnosing tumor, has
 PT specificity for activated cell surface receptor and binds specifically to
 PT an epitope that does not comprise phosphotyrosine residue.

XX Claim 53; Page 88; 114pp; English.

XX The present invention relates to novel antibodies, which have specificity
 CC for activated cell surface receptors (erbB, TNF and immunoglobulin gene
 CC superfamily: IgSF) and bind to an epitope (ABP59223-ABP59259). The
 CC antibodies are useful for preventing transformation of a normal cell into
 CC a tumour cell in a patient who had a tumour with tumour cells that
 CC express activated erbB receptors on the cell surface surgically removed
 CC or in whom the tumour has entered remission, for treating a patient
 CC suffering from a cancer characterised by tumour cells that have p185 on
 CC their cell surfaces, or for treating a patient suffering from an erbB
 CC tumour. The antibodies were produced by immunising a suitable host with a
 CC peptide (ABP59223-ABP59259), or its reverse sequence
 XX

SO Sequence 4 AA;

Query Match 86.7%; Score 13; DB 6; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 2 GSY 4

RESULT 15
 ADJ81984
 ID ADJ81984 standard; peptide; 4 AA.
 XX
 AC ADJ81984;
 XX

XX 06-MAY-2004 (first entry)
DT Thermus brockianus nucleic acid polymerase peptide fragment #2.
XX
DE nucleic acid polymerase; thermophile; mutation; exonuclease activity.
XX
KM Thermus brockianus.
XX
OS WO2003048308-A2.
XX
PN 12-JUN-2003.
XX
PD 22-NOV-2002; 2002WO-US037657.
XX
PF 30-NOV-2001; 2001US-0334434P.
XX
PR (APPL-) APPLERA CORP.
XX
PA Rozzelle J, Bolchakova E;
XX
PI WPI; 2003-505285/47.
XX
DR
XX
PT New Thermus brockianus nucleic acid polymerases, useful for DNA
PT synthesis, primer extension, DNA sequencing, reverse transcription, or
PT DNA and RNA amplification procedures.
XX
PS Disclosure; SEQ ID NO 18; 74pp; English.
XX
XX
CC The invention relates to novel nucleic acid polymerases from the
CC thermophilic organism Thermus brockianus or mutants having a mutation
CC that decreases 5'-3' exonuclease activity or reduces discrimination
CC against deoxynucleotide triphosphates. The nucleic acid polymerases,
CC kits are useful for DNA synthesis, primer extension, DNA sequencing,
CC reverse transcription, or DNA and RNA amplification procedures. The
CC nucleic acids are also useful for the recombinant expression of the
CC polymerase polypeptides. The nucleic acid polymerases and nucleic acids
CC are useful for the detection and isolation of nucleic acids encoding DNA
CC polymerase I activity. This sequence corresponds to a peptide of a
CC polymerase of the invention.
XX
SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 1 GAY 3

Search completed: December 13, 2004, 22:22:39
Job time : 80 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:12:37 ; Search time 21.4 Seconds
(without alignments)
12.396 Million cell updates/sec

Title: US-10-068-905-6

Perfect score: 15

Sequence: 1 GXY 4

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backlist.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	86.7	4	1	US-08-798-897-49
2	13	86.7	4	1	US-08-463-224-2
3	13	86.7	4	1	US-08-463-377-2
4	13	86.7	4	2	US-08-978-523-49
5	13	86.7	4	2	US-08-310-912A-199
6	13	86.7	4	3	US-09-301-085-199
7	13	86.7	4	5	PCT-US93-01669-41
8	13	86.7	4	5	PCT-US95-04589-199
9	13	86.7	5	1	US-07-963-569A-6
10	13	86.7	5	2	US-08-292-968-30
11	13	86.7	5	2	US-08-292-968-36
12	13	86.7	5	2	US-08-618-696-3
13	13	86.7	5	2	US-08-618-696-14
14	13	86.7	5	2	US-08-467-974-30
15	13	86.7	5	2	US-08-467-974-36
16	13	86.7	5	2	US-08-467-536-30
17	13	86.7	5	2	US-08-467-536-36
18	13	86.7	5	3	US-09-033-753-3
19	13	86.7	5	3	US-09-033-753-14
20	13	86.7	5	3	US-08-467-976-30
21	13	86.7	5	3	US-08-467-976-36
22	13	86.7	5	3	US-09-083-514-30
23	13	86.7	5	3	US-09-083-514-36
24	13	86.7	5	4	US-08-475-955-43
25	13	86.7	6	1	US-08-014-979-92
26	13	86.7	6	1	US-08-176-620A-21
27	13	86.7	6	1	US-08-248-538-20

28	13	86.7	6	1	US-08-248-538-40	Sequence 40, Appl
29	13	86.7	6	1	US-08-260-199A-31	Sequence 31, Appl
30	13	86.7	6	1	US-08-260-199A-32	Sequence 32, Appl
31	13	86.7	6	1	US-08-798-897-53	Sequence 53, Appl
32	13	86.7	6	1	US-08-690-605-21	Sequence 21, Appl
33	13	86.7	6	2	US-08-580-988A-16	Sequence 16, Appl
34	13	86.7	6	2	US-08-461-985-21	Sequence 21, Appl
35	13	86.7	6	2	US-08-978-523-53	Sequence 53, Appl
36	13	86.7	6	3	US-08-481-985B-132	Sequence 132, App
37	13	86.7	6	3	US-08-932-787B-12	Sequence 12, Appl
38	13	86.7	6	3	US-08-932-012C-12	Sequence 12, Appl
39	13	86.7	6	3	US-08-888-818C-12	Sequence 12, Appl
40	13	86.7	6	4	US-09-518-737-6	Sequence 6, Appl
41	13	86.7	6	6	5200320-19	Sequence 19, Appl
42	13	86.7	7	1	US-07-841-997A-19	Sequence 19, Appl
43	13	86.7	7	1	US-08-290-301-19	Sequence 19, Appl
44	13	86.7	7	2	US-09-070-756-8	Sequence 8, Appl
45	13	86.7	7	3	US-09-193-104-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-798-897-49
Sequence 49, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483, 0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-798-897-49

Query Match 86.7%; Score 13; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GAY 4

RESULT 2
US-08-463-224-2
Sequence 2, Application US/08463224
Patent No. 5807824
GENERAL INFORMATION:
APPLICANT: van Oostrom, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5807824Agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,224
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-224-2

Query Match 86.7%; Score 13; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GAY 4

RESULT 3
US-08-463-377-2
Sequence 2, Application US/08463377
Patent No. 5837499
GENERAL INFORMATION:
APPLICANT: van Oostrom, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5837499Agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,377
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-377-2

Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GAY 4

RESULT 4
US-08-978-523-49
Sequence 49, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Remond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2560
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-978-523-49

Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GAY 4

RESULT 5

US-08-310-912A-199
Sequence 199, Application US/08310912A
Patent No. 5961730
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumitaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310 912A
FILING DATE: September 22, 1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/227,360
FILING DATE: April 13, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/254001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-310-912A-199

Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GXY 3
DB 2 GAY 4

RESULT 6

US-09-301-085-199
Sequence 199, Application US/09301085
Patent No. 6262248
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumitaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
TITLE OF INVENTION: DETECTION METHODS
FILE REFERENCE: 00786/254002
CURRENT APPLICATION NUMBER: US/09/301,085
CURRENT FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: 08/310,912
EARLIER FILING DATE: 1994-09-22
EARLIER APPLICATION NUMBER: 08/227,360
EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 199
LENGTH: 4
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-301-085-199

Query Match 86.7%; Score 13; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GAY 4

RESULT 7

PCT-US93-01669-41
Sequence 41, Application PCT/US9301669
GENERAL INFORMATION:
APPLICANT: Trombridge, Ian S.
APPLICANT: Collawn, Jr., James F.
APPLICANT: Tainer, John A.
APPLICANT: Kuhn, Leslie A.
TITLE OF INVENTION: RECEPTOR INTERNALIZATION SIGNALS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Judas & Lubitz
STREET: 1860 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01669
FILING DATE: 01-MAR-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/844,852
FILING DATE: 03-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1636
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US93-01669-41

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GSY 4

RESULT 8
PCT-US95-04589-199
Sequence 199, Application PC/TUS9504589
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katsigiri, Purnaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04589
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04589-199

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GSY 4

RESULT 9
US-07-962-569A-6
Sequence 6, Application US/07962569A
Patent No. 5391497
GENERAL INFORMATION:
APPLICANT: MENON, RAVI S.
APPLICANT: JEFFERS, KATHLEEN F.
APPLICANT: CHANG, YING-PON
APPLICANT: HAM, RICHARD G.
TITLE OF INVENTION: HUMAN K-CASEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FREDERICK W. PEPPER, PH.D.
STREET: 11545 W. BERNARDO COURT, STE. 302
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92127
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/962,569A
FILING DATE: 19921013
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 920224.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 451-1120
TELEFAX: (619) 451-9628
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-962-569A-6

Query Match 86.7%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GSY 5

RESULT 10
US-08-292-968-30
Sequence 30, Application US/08292968
Patent No. 5656122
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COOMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney

```

/ STREET: Suite 701, 330 University Avenue
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,968
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 08/110,947
/ FILING DATE: 24-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/251,121
/ FILING DATE: 31-MAY-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: STEWART, Michael I.
/ REGISTRATION NUMBER: 24,973
/ REFERENCE/DOCKET NUMBER: 1038-388
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-292-968-30

Query Match      86.7%  Score 13; DB 2; Length 5;
Best Local Similarity 66.7%  Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GTY 4

RESULT 11
US-08-292-968-36
/ Sequence 36, Application US/08292968
/ Patent No. 5856122
/ GENERAL INFORMATION:
/ APPLICANT: READ, Randy J.
/ APPLICANT: STEIN, Penelope E.
/ APPLICANT: COCKLE, Stephen A.
/ APPLICANT: COOMEN, Raymond P.
/ APPLICANT: LOOSMORE, Sheena
/ APPLICANT: KLEIN, Michel H.
/ APPLICANT: ARMSTRONG, Glen D.
/ APPLICANT: HAZES, Bart
/ TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
/ NUMBER OF SEQUENCES: 46
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sim & McBurney
/ STREET: Suite 701, 330 University Avenue
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,968

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/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 08/110,947
/ FILING DATE: 24-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/251,121
/ FILING DATE: 31-MAY-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: STEWART, Michael I.
/ REGISTRATION NUMBER: 24,973
/ REFERENCE/DOCKET NUMBER: 1038-388
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-292-968-36

Query Match      86.7%  Score 13; DB 2; Length 5;
Best Local Similarity 66.7%  Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GTY 4

RESULT 12
US-08-618-696-3
/ Sequence 3, Application US/08618696
/ Patent No. 5861475
/ GENERAL INFORMATION:
/ APPLICANT: COOPER, Jr., J. ALLEN D.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
/ INHIBITION OF PHAGOCYTES
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ARNOLD, WHITE & DURKEE
/ STREET: P.O. BOX 4433
/ CITY: HOUSTON
/ STATE: TEXAS
/ COUNTRY: USA
/ ZIP: 77210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WORDPERFECT 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/618,696
/ FILING DATE: 20-MAR-1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/995,269
/ FILING DATE: 12/21/92
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PARKER, DAVID L.
/ REGISTRATION NUMBER: 32,165
/ REFERENCE/DOCKET NUMBER: UCAB:002/PAR
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-320-7200
/ TELEFAX: 512-474-7577
/ TEXT: NOT APPLICABLE
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acid residues
/ TYPE: amino acid
/ STRANDEDNESS: single

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TOPOLOGY: linear
US-08-618-696-3

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 1 GXY 3

RESULT 13

US-08-618-696-14
Sequence 14, Application US/08618696
Patent No. 5861475
GENERAL INFORMATION:
APPLICANT: COOPER, J., J. ALLEN D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
INHIBITION OF PHAGOCYTES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,696
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,269
FILING DATE: 12/21/92
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: USAB:002/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-618-696-14

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 1 GXY 3

RESULT 14
US-08-467-974-30
Sequence 30, Application US/08467974
Patent No. 5965385
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.

APPLICANT: COHEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,974
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-454 MIS:VJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-974-30

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GXY 4

RESULT 15
US-08-467-974-36
Sequence 36, Application US/08467974
Patent No. 5965385
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COHEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46

Tue Dec 14 10:04:27 2004

us-10-068-905-6.rat

Page 7

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sim & McBurney
;; STREET: Suite 701, 330 University Avenue
;; CITY: Toronto
;; STATE: Ontario
;; COUNTRY: Canada
;; ZIP: M5G 1R7
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/467,974
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/467,536
;; FILING DATE: 06-JUN-1995
;; APPLICATION NUMBER: US 08/292,968
;; FILING DATE: 22-AUG-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/251,121
;; FILING DATE: 31-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/110,947
;; FILING DATE: 24-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEWART, Michael I.
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-454 MIS:vg
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 36:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-467-974-36

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

Oy 1 GXY 3
Db 2 GTY 4

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Job time : 21.4 secs

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Tue Dec 14 10:04:28 2004

us-10-068-905-6.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:31:47 ; Search time 68.6 Seconds
(without alignments)

20.827 Million cell updates/sec

Title: US-10-068-905-6

Perfect score: 15

Sequence: 1 GXYX 4

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
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1	13	86.7	4	9	US-09-867-852-199	Sequence 199, App
2	13	86.7	4	14	US-10-302-817A-18	Sequence 18, App
3	13	86.7	4	15	US-10-613-472-199	Sequence 199, App
4	13	86.7	4	16	US-10-613-765-199	Sequence 199, App
5	13	86.7	5	10	US-09-792-686A-34	Sequence 34, App
6	13	86.7	5	14	US-10-344-779-8	Sequence 8, App
7	13	86.7	5	14	US-10-376-121A-143	Sequence 143, App
8	13	86.7	5	16	US-10-738-809-8	Sequence 8, App
9	13	86.7	5	16	US-10-394-471B-11	Sequence 3, App
10	13	86.7	5	16	US-10-394-471B-11	Sequence 11, App
11	13	86.7	6	9	US-09-990-762-36	Sequence 36, App
12	13	86.7	6	9	US-09-990-762-40	Sequence 40, App
13	13	86.7	6	9	US-09-990-762-41	Sequence 41, App

14	13	86.7	6	10	US-09-518-737-6	Sequence 6, App
15	13	86.7	6	10	US-09-858-852A-36	Sequence 36, App
16	13	86.7	6	10	US-09-858-852A-40	Sequence 40, App
17	13	86.7	6	10	US-09-858-852A-41	Sequence 41, App
18	13	86.7	6	14	US-10-285-046-23	Sequence 23, App
19	13	86.7	6	14	US-10-284-660-23	Sequence 23, App
20	13	86.7	6	15	US-10-394-980-232	Sequence 232, App
21	13	86.7	6	15	US-10-306-631-63	Sequence 63, App
22	13	86.7	6	15	US-10-435-751-108	Sequence 108, App
23	13	86.7	6	15	US-10-435-751-121	Sequence 121, App
24	13	86.7	6	15	US-10-133-234A-17	Sequence 17, App
25	13	86.7	6	15	US-10-133-234A-18	Sequence 18, App
26	13	86.7	6	15	US-10-133-234A-19	Sequence 19, App
27	13	86.7	6	15	US-10-133-234A-20	Sequence 20, App
28	13	86.7	6	15	US-10-133-234A-21	Sequence 21, App
29	13	86.7	6	16	US-10-415-014-732	Sequence 732, App
30	13	86.7	6	16	US-10-739-583-14	Sequence 14, App
31	13	86.7	6	17	US-10-813-638-1446	Sequence 1446, App
32	13	86.7	7	9	US-09-809-517A-15	Sequence 15, App
33	13	86.7	7	10	US-09-792-686A-31	Sequence 31, App
34	13	86.7	7	14	US-10-286-457-129	Sequence 129, App
35	13	86.7	7	14	US-10-286-457-189	Sequence 189, App
36	13	86.7	7	15	US-10-398-104-326	Sequence 326, App
37	13	86.7	7	17	US-10-741-481-35	Sequence 35, App
38	13	86.7	8	9	US-09-765-086-157	Sequence 157, App
39	13	86.7	8	9	US-09-756-283A-59	Sequence 59, App
40	13	86.7	8	9	US-09-756-283A-97	Sequence 97, App
41	13	86.7	8	9	US-09-562-445-15	Sequence 15, App
42	13	86.7	8	9	US-09-910-552-22	Sequence 22, App
43	13	86.7	8	10	US-09-880-748-3084	Sequence 3084, App
44	13	86.7	8	14	US-10-264-374-157	Sequence 157, App
45	13	86.7	8	14	US-10-375-992-157	Sequence 157, App

ALIGNMENTS

RESULT 1
US-09-867-852-199
Sequence 199, Application US/09867852
Patent No. US2002014732A1
GENERAL INFORMATION:
APPLICANT: Amshel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Rumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
FILE REFERENCE: DETECTION METHODS
CURRENT APPLICATION NUMBER: US/09/867,852
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 199
LENGTH: 4
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-867-852-199
Query Match 86.7%; Score 13; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 2

US-10-302-817A-18
; Sequence 18, Application US/10302817A
; Publication No. US20030198978A1
; GENERAL INFORMATION:
; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768US
; CURRENT APPLICATION NUMBER: US/10/302,817A
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: 60/334,434
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Thermus brockianus
US-10-302-817A-18

Query Match 86.7%; Score 13; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 1 GAY 3

RESULT 3

US-10-613-472-199
; Sequence 199, Application US/10613472
; Publication No. US20040088756A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Stasiewicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254004
; CURRENT APPLICATION NUMBER: US/10/613,472
; PRIOR FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 09/867,852
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/301,085
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: US 08/310,912
; PRIOR FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: US 08/227,360
; PRIOR FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-472-199

Query Match 86.7%; Score 13; DB 15; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 4

US-10-613-765-199
; Sequence 199, Application US/10613765
; Publication No. US20040172673A1
; GENERAL INFORMATION:
; APPLICANT: AUSUBEL, FREDERICK M.
; APPLICANT: STASIEWICZ, BRIAN J.
; APPLICANT: KATAGIRI, FUMIYUKI
; APPLICANT: KUNKEL, BARBARA N.
; APPLICANT: MINDINOS, MICHAEL N.
; APPLICANT: YU, GUO-LIANG
; APPLICANT: BAKER, BARBARA
; APPLICANT: ELIUS, JEFFREY
; APPLICANT: SALMERON, JOHN
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254005
; CURRENT APPLICATION NUMBER: US/10/613,765
; PRIOR FILING DATE: 2003-07-02
; CURRENT APPLICATION NUMBER: US 09/867,852
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/301,085
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: US 08/310,912
; PRIOR FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: US 08/227,360
; PRIOR FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-765-199

Query Match 86.7%; Score 13; DB 16; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 5

US-09-792-686A-34
; Sequence 34, Application US/09792686A
; Publication No. US20030068645A1
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Kopecky, Stephen L.
; APPLICANT: Weyand, Cornelia M.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR EVALUATING
; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
; FILE REFERENCE: 07039-250001
; CURRENT APPLICATION NUMBER: US/09/792,686A
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-686A-34

Query Match 86.7%; Score 13; DB 10; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Tue Dec 14 10:04:28 2004

us-10-068-905-6.rapb

Page 3

OY 1 GXY 3
DB 3 GTY 5

RESULT 6

US-10-344-779-8
; Sequence 8, Application US/103444779
; Publication No. US200302110661
; GENERAL INFORMATION:
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TORNETTA, MARK A.
; APPLICANT: TRUENH, ALMESEGED
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
; FILE REFERENCE: GPE0033
; CURRENT APPLICATION NUMBER: US/10/344,779
; CURRENT FILING DATE: 2003-02-17
; PRIOR APPLICATION NUMBER: PCT/US01/26161
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,524
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/230,639
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-344-779-8

Query Match 86.7%; Score 13; DB 14; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7

US-10-376-121A-143
; Sequence 143, Application US/10376121A
; Publication No. US200302165441
; GENERAL INFORMATION:
; APPLICANT: HARLEY, JOHN
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patricia L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991

APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: CMRPL14CIP(2) DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 143:

US-10-376-121A-143

Query Match 86.7%; Score 13; DB 14; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8

US-10-738-809-8
; Sequence 8, Application US/10738809
; Publication No. US2004017117A1
; GENERAL INFORMATION:
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TORNETTA, MARK A.
; APPLICANT: TRUENH, ALMESEGED
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
; FILE REFERENCE: GPE0033
; CURRENT APPLICATION NUMBER: US/10/738,809
; CURRENT FILING DATE: 2003-12-17
; PRIOR APPLICATION NUMBER: US/10/344,779
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US01/26161
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,524
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/230,639
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-738-809-8

Query Match 86.7%; Score 13; DB 16; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
DB 1 GTY 3

RESULT 9

US-10-394-471B-3
; Sequence 3, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
; APPLICANT: GILES-KOMAR, JILL; CARTON, JILL; SCALLON, BERNARD J.

```

; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0202
; CURRENT APPLICATION NUMBER: US/10/394,471B
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/367,903
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-471B-3

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Query Match
Best Local Similarity 86.7%; Score 13; DB 16; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GXY 3
| |
Db 2 GSY 4

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RESULT 10
US-10-394-471B-11
; Sequence 11, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill; Carton, Jill; Scallion, Bernard J.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0202
; CURRENT APPLICATION NUMBER: US/10/394,471B
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/367,903
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-471B-11

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Query Match
Best Local Similarity 86.7%; Score 13; DB 16; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 GXY 3
| |
Db 2 GSY 4

```

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RESULT 11
US-09-990-762-36
; Sequence 36, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-990-762-36

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Query Match
Best Local Similarity 86.7%; Score 13; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GXY 3
| |
Db 3 GAY 5

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RESULT 12
US-09-990-762-40
; Sequence 40, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-990-762-40

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Query Match
Best Local Similarity 86.7%; Score 13; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GXY 3
| |
Db 3 GAY 5

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RESULT 13
US-09-990-762-41
; Sequence 41, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
OTHER INFORMATION: recognition sequence
US-09-990-762-41

Query Match
Best Local Similarity 86.7%; Score 13; DB 9; Length 6;
Matches 2; Conservative 0; Pred. No. 1.4e+06; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GAY 5

RESULT 14
US-09-518-737-6
Sequence 6, Application US/09518737
Publication No. US2003008321A1
GENERAL INFORMATION:
APPLICANT: FUKUI, YASUHISA
APPLICANT: NAGATA, SATOSHI
APPLICANT: SHIRAI, RYUICHI
APPLICANT: SAITO, NAOKI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE
FILE REFERENCE: 1965/49618
CURRENT APPLICATION NUMBER: US/09/518,737
PRIOR APPLICATION NUMBER: 2000-03-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 6
TYPE: PRT
ORGANISM: Mus musculus
US-09-518-737-6

Query Match 86.7%; Score 13; DB 10; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GSY 6

RESULT 15
US-09-858-852A-36
Sequence 36, Application US/09858852A
Publication No. US20030044787A1
GENERAL INFORMATION:
APPLICANT: JOUNG, J. KEITH
APPLICANT: MILLER, JEFFREY
APPLICANT: PAHO, CARL O.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
FILE REFERENCE: MTV-030.01 (20021-3001)
CURRENT APPLICATION NUMBER: US/09/858,852A
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/204,509
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 36
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
OTHER INFORMATION: recognition sequence
US-09-858-852A-36

Query Match 86.7%; Score 13; DB 10; Length 6;

Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GAY 5

Search completed: December 13, 2004, 23:02:39
Job time : 68.6 secs

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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:01:21 ; Search time 15.2 Seconds
(without alignments)
25.320 Million cell updates/sec

Title: US-10-068-905-6

Perfect score: 15

Sequence: 1 GYX 4

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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
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2	13	86.7	9	2	G41946
3	13	86.7	11	2	PT0250
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6	13	86.7	12	2	S47391
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8	13	86.7	12	2	PH1611
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10	13	86.7	12	2	PH0790
11	13	86.7	13	2	S47368
12	13	86.7	13	2	S47383
13	13	86.7	13	2	PH0788
14	13	86.7	13	2	PH0700
15	13	86.7	14	2	AS9018
16	13	86.7	14	2	PH1601
17	13	86.7	14	2	PH0792
18	13	86.7	15	2	PH1582
19	13	86.7	16	2	S11290
20	13	86.7	17	2	S48655
21	13	86.7	17	2	A60317
22	13	86.7	17	2	R35141
23	13	86.7	18	2	I73024
24	13	86.7	18	2	PH1629
25	13	86.7	19	2	PH1609
26	13	86.7	20	2	FX0059
27	13	86.7	20	2	JA0142
28	13	86.7	20	2	A54519
29	13	86.7	20	2	PI0161

30	13	86.7	20	2	S44455	pyrithocorticin - Py
31	13	86.7	21	2	PI0227	Ig heavy chain CDR
32	13	86.7	21	2	S47198	T-cell receptor J-
33	13	86.7	21	2	S47212	T-cell receptor J-
34	13	86.7	22	2	PH1680	Ig heavy chain V r
35	13	86.7	22	2	A53794	lycoidine synthas
36	13	86.7	23	2	A53631	H+-transporting tw
37	13	86.7	23	2	PH1725	Ig heavy chain V r
38	13	86.7	24	2	I73584	alpha 1-proteinase
39	13	86.7	24	2	I61491	seed protein ws-9
40	13	86.7	24	2	D27579	T-cell receptor be
41	13	86.7	24	2	A05298	fibrinogen gamma c
42	13	86.7	24	2	A45087	cysteine proteinas
43	13	86.7	25	2	S56000	guanidino kinase M
44	13	86.7	25	2	A58647	alpha-conotoxin P
45	13	86.7	26	2	PI0105	alkaline serine pr

ALIGNMENTS

RESULT 1
S36850
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C/Accession: S36850
R/Jacob, J.; Kelsoe, G.
Submitted to the EMBL Data Library, July 1992
A/Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophen

A/Reference number: S25024
A/Accession: S36850
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-9 <JAC>
A/Cross-references: EMBL:X67387; NID:G50113; PIDN:CAA47799.1; PID:G51594; PID:G1333871
C/Keywords: heterotrimer; immunoglobulin

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 9;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYX 3
DB 6 GSY 8

RESULT 2
G41946
T-cell receptor gamma chain (2t.23) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C/Accession: G41946

R/Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A/Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma g
A/Reference number: A41946; MUID:92049316; PMID:1658619
A/Accession: G41946

A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-9 <WHB>
C/Keywords: T-cell receptor

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 9;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYX 3
DB 3 GSY 5

RESULT 3

PT0250
 Ig heavy chain CRD3 region (clone 2-109B) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0250
 R/Yamada, M.; Messerman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Royera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
 A/Reference number: PT0222; PMID:91108337; PMID:1899102
 A/Accession: PT0250
 A/Molecule type: DNA
 A/Residues: 1-11 <YAM>
 A/Experimental source: B lymphocyte
 C/Keywords: heterotetramer; immunoglobulin

Query Match 86.7%; Score 13; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 Db 1 GTY 3

RESULT 4
 PT0214
 T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
 C/Accession: PT0214
 R/Nakano, N.; Kikurani, H.; Nishimoto, H.; Kishimoto, T.
 J. Exp. Med. 173, 1091-1097, 1991
 A/Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted
 A/Reference number: PT0209; PMID:91217621; PMID:1902501
 A/Accession: PT0214
 A/Molecule type: mRNA
 A/Residues: 1-11 <NAK>
 C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 8.1e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 Db 5 GTY 7

RESULT 5
 A33099
 163K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
 C/Species: Plasmodium falciparum
 C/Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C/Accession: A33099
 R/Nichols, J.H.; Hager, L.P.
 Submitted to the Protein Sequence Database, May 1990
 A/Reference number: A33098
 A/Accession: A33099
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-12 <NTC>

Query Match 86.7%; Score 13; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 Db 9 GTY 11

RESULT 6
 S47391

T-cell antigen receptor VJ junction beta chain - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C/Accession: S47391, S47386
 R/Lehner, P.U.
 Submitted to the EMBL Data Library, August 1994
 A/Description: Human HLA-A*0201 restricted recognition of Influenza A is dominated by T
 A/Reference number: S47395
 A/Accession: S47391
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-12 <LEH>
 A/Cross-references: EMBL:Z35712; NID:G527519; PIDN:CAA84781.1; PID:G527520; EMBL:Z35701
 C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 Db 6 GSY 8

RESULT 7
 S47395
 T-cell antigen receptor VJ junction beta chain - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C/Accession: S47395
 R/Lehner, P.U.
 Submitted to the EMBL Data Library, August 1994
 A/Description: Human HLA-A*0201 restricted recognition of Influenza A is dominated by T
 A/Reference number: S47355
 A/Accession: S47395
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-12 <LEH>
 A/Cross-references: EMBL:Z35715; NID:G527525; PIDN:CAA84784.1; PID:G527526
 C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 Db 6 GSY 8

RESULT 8
 PH1611
 Ig H chain V-D-J region (wild-type clone 341) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1611
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A/Reference number: PH1580; PMID:93301609; PMID:8315387
 A/Accession: PH1611
 A/Molecule type: DNA
 A/Residues: 1-12 <LEV>
 A/Experimental source: bone marrow pre-B lymphocyte
 C/Keywords: immunoglobulin

Query Match 86.7%; Score 13; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 Db 5 GSY 7

RESULT 9
PH0802
T-cell receptor alpha chain (M2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0802
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0802
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X60910
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 6 GTY 8

RESULT 10
PH0790
T-cell receptor alpha chain (OB7.3.2 V-alpha-4.3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0790
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0790
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X60895
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 6 GTY 8

RESULT 11
S47368
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47368
R/Lehner, P.U.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A/Reference number: S47355
A/Accession: S47368
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:X25693; NID:9527477; PIDN:CAA84762.1; PID:9527478
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 7 GAY 9

RESULT 12
S47383
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47383
R/Lehner, P.U.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A/Reference number: S47355
A/Accession: S47383
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:X25709; NID:9527513; PIDN:CAA84778.1; PID:9527514
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 7 GSY 9

RESULT 13
PH0788
T-cell receptor alpha chain (E22 V-alpha-8.F3.4) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0788
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0788
A/Molecule type: mRNA
A/Residues: 1-13 <CAS>
A/Cross-references: EMBL:X60893
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 7 GTY 9

RESULT 14
P00700
Unidentified 6.3/40K protein [imported] - rice (fragment)
C/Species: Oryza sativa (rice)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: P00700
R/Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A/Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A/Reference number: P00696
A/Accession: P00700

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <KOW>
A:Cross-references: UNIPROT:Q7MU1

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 3 GAY 5

RESULT 15

A59018
MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
C/Accession: A59018
R/Abel, M.; Smith, C.J.; Larson, C.J.
A/Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a breast cancer cell line MCF-7
A/Reference number: A59018
A/Accession: A59018
A:Molecule type: protein
A/Residues: 1-14 <ABE>
A/Experimental source: breast cancer cell line MCF-7
A/Note: 3-Val was also found
C/Keywords: DNA binding; heterodimer

Query Match 86.7%; Score 13; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 6 GSY 8

Search completed: December 13, 2004, 22:32:59
Job time : 16.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:00:41; Search time 83.8 Seconds

(without alignments)
27.464 Million cell updates/sec

Title: US-10-068-905-6
Perfect score: 15
Sequence: 1 GXY 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	86.7	8	1 UP06_MOUSE	P38644 mus musculu
2	13	86.7	9	2 Q9QWTO	Q9QWTO mus musculu
3	13	86.7	10	3 Q9NEX9	Q9NEX9 homo sapien
4	13	86.7	10	4 AAO63472	AAO63472 homo sapi
5	13	86.7	11	2 Q9UC46	Q9UC46 homo sapien
6	13	86.7	11	2 Q7YPC2	Q7YPC2 homo sapien
7	13	86.7	13	1 ADFB_TENMO	P83109 tenebrilio m
8	13	86.7	13	2 P82432	P82432 nicotiana t
9	13	86.7	13	2 Q7YOR1	Q7YOR1 oryza sativ
10	13	86.7	13	2 Q7YOR1	Q7YOR1 brassica ju
11	13	86.7	15	1 PH3_PRUSE	P29265 prunus sero
12	13	86.7	15	1 UCL4_MAIZE	P80620 zea mays (m
13	13	86.7	15	2 Q9SEI4	Q9SEI4 zea mays (m
14	13	86.7	15	2 Q47892	Q47892 firemyella d
15	13	86.7	15	2 Q47893	Q47893 firemyella d
16	13	86.7	16	1 PH2_PRUSE	P29264 prunus sero
17	13	86.7	16	2 Q7LGD2	Q7LGD2 homo sapien
18	13	86.7	16	2 Q6JDK5	Q6JDK5 canis famli
19	13	86.7	16	2 Q9SMW3	Q9SMW3 aradidopsi
20	13	86.7	17	2 Q6LCL9	Q6LCL9 aradidopsi
21	13	86.7	17	2 Q6Z645	Q6Z645 saguinus oe
22	13	86.7	17	2 Q7IVQ4	Q7IVQ4 homo sapien
23	13	86.7	17	2 Q9T2H6	Q9T2H6 spiniacia ol
24	13	86.7	17	2 Q84098	Q84098 influenza a
25	13	86.7	17	2 Q7LZNI	Q7LZNI torpedo mar
26	13	86.7	17	2 AAC39714	AAC39714 homo sapi
27	13	86.7	17	2 AAB92363	AAB92363 homo sapi
28	13	86.7	18	2 Q9GJW1	Q9GJW1 lagenorhinc
29	13	86.7	18	2 Q9GJW2	Q9GJW2 lagenorhinc
30	13	86.7	18	2 Q9GJW3	Q9GJW3 lagenorhinc
31	13	86.7	18	2 Q6LD78	Q6LD78 clostridium

32	13	86.7	18	2 Q9R4C6	Q9R4C6 agrobacteri
33	13	86.7	18	2 Q9R4F9	Q9R4F9 aeromonas.
34	13	86.7	18	2 Q9R501	Q9R501 bacillus su
35	13	86.7	18	2 Q9PRX1	Q9PRX1 structlio ca
36	13	86.7	18	2 Q9R893	AAB20893 clostridi
37	13	86.7	19	2 Q9N613	Q9N613 toxoplasma
38	13	86.7	19	2 Q9GNL6	Q9GNL6 drosophila
39	13	86.7	19	2 Q47895	Q47895 firemyella d
40	13	86.7	19	2 Q9R4F8	Q9R4F8 aeromonas.
41	13	86.7	19	2 Q9R4F8	Q9R4F8 aeromonas.
42	13	86.7	20	1 PYRR_PRRAP	Q9F518 yersinia pe
43	13	86.7	20	2 Q25281	P37362 pyrrhocoris
44	13	86.7	20	2 Q9GNL7	Q25281 leishmania
45	13	86.7	20	2 Q9S8H8	Q9GNL7 drosophila
					Q9S8H8 brassica na

ALIGNMENTS

RESULT 1
ID UP06_MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RA MEDLINE=95009907; PubMed=7523108;
RX Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.2, its Mw is: 50 kDa.
KW Direct protein sequencing.
FT NON TER
SQ SEQUENCE 8 AA; 817 MW; A35DD87867B05B1 CRC64;

Query Match 86.7%; Score 13; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 6 GAY 8

RESULT 2
ID Q9QWTO PRELIMINARY; PRT; 9 AA.
AC Q9QWTO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Proteinase 3 (Myeloblastin) (Fragment).
GN Name=Prt3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=SV129 D3;
RA Lutz P.G., Moog-Lutz C., Houzel-Charavel A., Cayre Y.E.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AJ007030; CAA07429.1; -

DR MGD, MGI:893580; Prcn3.
FT NON TER 9
SQ SEQUENCE 9 AA; 937 MW; C91E75A77B45B87D CRC64;

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 9;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GSY 5

RESULT 3

Q8NEV9 PRELIMINARY; PRT; 10 AA.
AC Q8NEV9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Type II hair-specific keratin (Type II hair keratin) (Fragment).
GN Name=KRT8B;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Baitwa N.K., Bamezai R.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Baitwa N.K., Bamezai R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY037552; AK68688.1;
DR EMBL: AY203963; AA063472.1;
DR GO: GO:0005882; C:intermediate filament; IEA.
KW Keratin.
FT NON TER 10
SQ SEQUENCE 10 AA; 1034 MW; 9B53417EAB45B87E CRC64;

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 10;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GSY 6

RESULT 4
AA063472 PRELIMINARY; PRT; 10 AA.
AC AA063472;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Type II hair keratin (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Baitwa N.K., Bamezai R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY203963; AA063472.1;
KW Keratin.
FT NON TER 10
SQ SEQUENCE 10 AA; 1034 MW; 9B53417EAB45B87E CRC64;

Query Match 86.7%; Score 13; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GSY 6

RESULT 5

Q9UC46 PRELIMINARY; PRT; 11 AA.
AC Q9UC46;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Neutrophil inhibitor peptide, NIP=POLYMORPHONUCLEAR neutrophil inhibitor peptide.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=9636114; PubMed=8703476;
RA Cooper J.A., Jr.; Culbreth R.R.;
RT "Characterization of a neutrophil inhibitor peptide harvested from human bronchial lavage: homology to influenza A nucleoprotein."
RL Am. J. Respir. Cell Mol. Biol. 15:207-215(1996).
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0030236; P:anti-inflammatory response; NAS.
SQ SEQUENCE 11 AA; 1262 MW; 951AC3279C9DB45 CRC64;

Query Match
Best Local Similarity 66.7%; Score 13; DB 2; Length 11;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GSY 5

RESULT 6
Q7YP62 PRELIMINARY; PRT; 11 AA.
AC Q7YP62;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MHC class Ib antigen (Fragment).
GN Name=HLA-F;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., He X., Xu L., Zeng Y.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY285156; AAP94210.1;
FT NON TER 11
SQ SEQUENCE 11 AA; 1208 MW; 2E0B6C5CC5AB45B8 CRC64;

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 11;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GSY 6

RESULT 7
ADFB_TENMO

ID ADFB TENMO STANDARD; PRT; 13 AA.
 AC P83109;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DS Antidiuretic Factor B (ADFB).
 OS Antidiuretic Factor B (ADFB).
 OC Tenebrio molitor (Yellow mealworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tenebrio.
 OC NCBI_TaxID=7067;
 RN [1]
 RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
 RP SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=22465067; PubMed=12576082;
 RA Eigenheer R.A., Niehart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,
 RA Hull J.J., Schooley D.A.;
 RT "Isolation, identification and localization of a second beetle
 RT antidiuretic peptide.";
 RL Peptides 24:27-34(2003).
 CC -1- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses
 CC CGMP as second messenger. May function as an antidiuretic hormone.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two
 CC pairs of bilaterally symmetrical cells in the protocerebrum.
 CC -1- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI; RANGE=1-13;
 CC NOTE=Ref.1.
 KW DIRECT protein sequencing; Hormone; Neuropeptide.
 SQ SEQUENCE 13 AA; 1562 MW; 0240A45048BA632B CRC64;

Query Match 86.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 4 GSY 6

RESULT 8
 ID P82432 PRELIMINARY; PRT; 13 AA.
 AC P82432;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DS 32 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Botwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture";
 RL Planta 0:0-0(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL.
 CC -1- TISSUE SPECIFICITY: XYLEM.
 DR GO; GO:0005618; C:cell wall; IEA.
 KW Cell wall.
 FT NON_TER
 SQ SEQUENCE 13 AA; 1307 MW; D5022297D8697DC6 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3

DB 9 GAY 11

RESULT 9
 ID 07M1U1 PRELIMINARY; PRT; 13 AA.
 AC 07M1U1;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Unidentified 6.3/40K protein (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RA Komatsu S., Kajiwara H., Hirano H.;
 RT "A rice protein library; a data-file of rice proteins separated by
 RT two-dimensional electrophoresis.";
 RL Theor. Appl. Genet. 86:935-942(1993).
 DR PIR; PQ0700; PQ0700.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 13 AA; 1218 MW; 27EA7291E7D3D878 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 3 GAY 5

RESULT 10
 ID 07Y0R1 PRELIMINARY; PRT; 13 AA.
 AC 07Y0R1;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Gamma-glutamylcysteine synthetase (EC 6.3.2.2) (Fragment).
 GN Name=gsh1;
 OS Brassica juncea (leaf mustard) (Indian mustard).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Brassica.
 OC NCBI_TaxID=3707;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wächter A., Steining H., Rausch T., Bogs J.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ564376; CAD91995.1;
 DR GO; GO:0004357; F:glutamate-cysteine ligase activity; IEA.
 KW ligase.
 FT NON_TER
 SQ SEQUENCE 13 AA; 1266 MW; DBF2097182417DC6 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 9 GAY 11

RESULT 11
 PH3_PRUSE

ID PH3 PRUSE STANDARD; PRT; 15 AA.
 AC P29265;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Prunasin beta-glucosidase IIB (EC 3.2.1.118) (Prunasin hydrolase
 isozyme IIB) (PH IIB) (Fragment).
 OS Prunus serotina (Black cherry).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosid1; Rosales; Rosaceae; Amygdaloideae; Prunus.
 NCBI_TaxID=23207;
 RX SEQUENCE.
 RP TISSUE=Seed;
 RA Li C.P., Swain E., Poulton J.E.;
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
 RL Plant Physiol. 100:282-280(1992).
 CC -1- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-
 glucose.
 CC -1- SUBUNIT: Monomer.
 CC -1- DEVELOPMENTAL STAGE: Absent from maturing black cherry fruits
 until 6 weeks after flowering. Then, concomitant with cotyledon
 development, the level of enzyme increases with specificity for
 embryonal tissues.
 CC -1- PTM: Glycosylated.
 KW Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
 KM Multigene family.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1635 MM; 4F3D7F4FB9CFC64 CRC64;

Query Match 86.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 Db 1 GTY 3

RESULT 12
 ID UC14 MAIZE STANDARD; PRT; 15 AA.
 AC P80620;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 258)
 DE (Fragment).
 OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACCD clade; Panicoideae; Andropogonaceae; Zea.
 NCBI_TaxID=4377;
 RX SEQUENCE.
 RP TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Perrotier J.-C., Zivy M., de Vienne P.;
 RT "The maize two dimensional gel protein database: towards an integrated
 genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996)
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 protein is: 5.9, its MW is: 34.6 kDa.
 DR Maize2DB; P80620; COLEOPTILE.
 DR Maize2DB; 123944; -;
 KW Direct protein sequencing.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1564 MM; CF0BBA0B7DB6658 CRC64;

Query Match 86.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 Db 7 GAY 9
 RESULT 13
 ID Q9S8L4 PRELIMINARY; PRT; 15 AA.
 AC Q9S8L4;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Beta-D-glucoside glucosylase (EC 3.2.1.21) (Fragment).
 OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACCD clade; Panicoideae; Andropogonaceae; Zea.
 NCBI_TaxID=4577;
 RX SEQUENCE.
 RP MEDLINE=94347094; PubMed=8068000;
 RA Feldwisch J., Vente A., Zetl R., Bako L., Campos N., Palme K.;
 RT "Characterization of two membrane-associated beta-glucosidases from
 maize (Zea mays L.) coleoptiles.";
 RL Biochem. J. 302:15-21(1994)
 DR GO; GO:0008422; F:beta-glucosidase activity; IEA.
 SQ SEQUENCE 15 AA; 1667 MM; 46C40370C8C730B CRC64;

Query Match 86.7%; Score 13; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 Db 3 GSY 5

RESULT 14
 ID Q47892 PRELIMINARY; PRT; 15 AA.
 AC Q47892;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Beta-allylphycocyanin (Fragment).
 OS Fremyella diplospion (Calothrix PCC 7601).
 CC Bacteria; Cyanobacteria; Nostocales; Microthetaceae; Fremyella.
 NCBI_TaxID=1197;
 RX SEQUENCE FROM N.A.
 RP MEDLINE=66233345; PubMed=3086870;
 RA Conley P.B., Iemaux P.G., Lomax T.L., Grossman A.R.;
 RT "Genes encoding major light-harvesting polypeptides are clustered on
 the genome of the cyanobacterium Fremyella diplospion.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928(1986).
 DR EMBL; M13216; AAA24871.1; -;
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1644 MM; 97271656699F462F CRC64;

Query Match 86.7%; Score 13; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 Db 4 GSY 6

RESULT 15
 ID Q47893 PRELIMINARY; PRT; 15 AA.

AC Q47893;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Beta-phyocyanin (Fragment).
 OS Fremyella diplosiphon (Calothrix PCC 7601).
 OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
 OX NCBI_Taxid=1197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66233345; PubMed=3086870;
 RA Conley F.B., Lemaux P.G., Lomax T.L., Grossman A.R.;
 RT "Genes encoding major light-harvesting polypeptides are clustered on
 the genome of the cyanobacterium Fremyella diplosiphon.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928(1986).
 DR EMBL; M13217; AAA24880.1; -
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1528 MM; 7FF2P65518F493D4 CRC64;
 Query Match 86.7%; Score 13; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GXY 3
 Db 4 GSY 6

Search completed: December 13, 2004, 22:31:36
 Job time : 83.8 secs

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OM protein - protein search, using sw model

Run on: December 13, 2004, 21:59:41 ; Search time 80 Seconds
(without alignments)
17.936 Million cell updates/sec

Title: US-10-068-905-7

Perfect score: 15

Sequence: 1 GXYX 4

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseq_23Sep04:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003as:*
8: Geneseqp2003bs:*
9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	86.7	4	1 AAP61656	Aap61656 Sequence
2	13	86.7	4	1 AAP71313	Aap71313 Peptide c
3	13	86.7	4	2 AAR55333	Aar55333 Inhibitor
4	13	86.7	4	2 AAR75499	Aar75499 Csa recep
5	13	86.7	4	5 ABP55713	Abp55713 B15 class
6	13	86.7	4	5 ABP55796	Abp55796 B15 class
7	13	86.7	4	5 ABG96845	Abg96845 Human leu
8	13	86.7	4	5 ABG97024	Abg97024 Human leu
9	13	86.7	4	5 ABG96697	Abg96697 Human leu
10	13	86.7	4	5 ABP67652	Abp67652 Human CD6
11	13	86.7	4	5 ABP67653	Abp67653 Human CD6
12	13	86.7	4	5 AAB84247	Aab84247 Caspase c
13	13	86.7	4	6 ABJ18638	Abj18638 ErbB rece
14	13	86.7	4	6 ABP59243	Abp59243 Peptide e
15	13	86.7	4	7 ADL98388	Adl98388 Thernus b
16	13	86.7	4	7 ADL98388	Adl98388 Human leu
17	13	86.7	4	7 ADL98369	Adl98369 Human leu
18	13	86.7	4	7 ADL98514	Adl98514 Human leu
19	13	86.7	4	7 ADL98678	Adl98678 Human leu
20	13	86.7	4	8 ADK42069	Adk42069 Antipace
21	13	86.7	4	8 ADK42068	Adk42068 Antipace
22	13	86.7	5	2 AAR43432	Aar43432 Ro/SSA ep
23	13	86.7	5	2 AAR6301	Aar6301 Second ge
24	13	86.7	5	2 AAR56298	Aar56298 Synthetic
25	13	86.7	5	2 AAR72555	Aar72555 Pertussis

26	13	86.7	5	2 AAR72549	Aar72549 Pertussis
27	13	86.7	5	2 AAR72699	Aar72699 Kappa-cas
28	13	86.7	5	2 AAY1820	Aay1820 Pertussis
29	13	86.7	5	2 AAY1826	Aay1826 Pertussis
30	13	86.7	5	2 AAW95230	Aaw95230 PT toxin
31	13	86.7	5	2 AAW95236	Aaw95236 PT toxin
32	13	86.7	5	2 AAY43373	Aay43373 Pertussis
33	13	86.7	5	2 AAY43367	Aay43367 Pertussis
34	13	86.7	5	3 AAY44679	Aay44679 Hydroporo
35	13	86.7	5	3 AAY68369	Aay68369 Pertussis
36	13	86.7	5	3 AAY68375	Aay68375 Pertussis
37	13	86.7	5	3 AAB08397	Aab08397 Peptide d
38	13	86.7	5	3 AAB66243	Aab66243 B pertuss
39	13	86.7	5	4 AAB66249	Aab66249 B pertuss
40	13	86.7	5	5 ABP67641	Abp67641 Human CD6
41	13	86.7	5	5 ABP67642	Abp67642 Human CD6
42	13	86.7	5	5 AAE16333	Aae16333 N-termina
43	13	86.7	5	5 ABB75621	Abb75621 Anti-RANK
44	13	86.7	5	5 ABJ18639	Abj18639 ErbB rece
45	13	86.7	6	6 ABP59244	Abp59244 Peptide e

ALIGNMENTS

RESULT 1	
AAP61656	
ID	AAP61656 standard; protein; 4 AA.
XX	
AC	AAP61656;
XX	
DT	25-MAR-2003 (revised)
DT	03-OCT-2002 (revised)
DT	21-AUG-1991 (first entry)
DE	Sequence of peptide which inhibits cyclic-nucleotide independent protein
DE	kinase activity and mammalian cell growth.
XX	
KW	Cell growth inhibitor; tumour cell growth inhibitor.
OS	Synthetic.
XX	
FT	Key
FT	Misc-difference 1 Location/Qualifiers
FT	Misc-difference 4 /label= Carbobenzoxy-Phe
FT	Misc-difference 4 /label= Tyr-CH2Cl
XX	
PN	US4582821-A.
XX	
PD	15-APR-1986.
XX	
PF	16-NOV-1983; 83US-00552255.
XX	
FR	16-NOV-1983; 83US-00552255.
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	
PI	Ketner CA, Racker E;
XX	
PS	WPI, 1986-118872/18.
DR	
XX	
PT	Inhibition of tumour cell growth - using peptide and aminoacid
PT	halo:methyl ketone(s).
XX	
PS	Claim 1; Col 4; 9pp; English.
XX	
CC	The cpds. of the invention inhibit protein phosphorylation. The inventors
CC	claim a process for inhibiting the growth of tumour cells in a medium
CC	which comprises contacting the cells with a cpd. of formula (AAP61654-
CC	P61661) or a physiologically acceptable salt. (Updated on 03-OCT-2002 to
CC	add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

PI Van Oostrum J, Boyar WC, Galakatos NG, Peppard JV;
XX
DR WPI, 1995-224319/29.
XX
PT C5a receptor antagonists having no agonist activity - are used in
XX compns. to treat C5a-mediated diseases and inflammatory conditions.
XX
PS Disclosure; Page 36; 65pp; English.
XX
CC Polypeptide receptor antagonists to C5a contain an essential core
CC tetrapeptide (AAR75498 or AAR5499) or core tripeptide (DGA) which
CC displays C5a blocking activity. (Updated on 25-MAR-2003 to correct FN
CC field.)
XX
SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| | |
2 GAY 4

Db

RESULT 5
ABP55713
ID ABP55713 standard; peptide; 4 AA.
XX
AC ABP55713;
XX
DT 25-FEB-2003 (first entry)
XX
DE B15 class I sHLA molecule ligand related peptide #7.
XX
KW HLA ligand; human leukocyte antigen; predictive algorithm; database;
KM MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
XX
OS Synthetic.
XX
PN WO200269198-A2.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005298.
XX
PR 21-FEB-2001; 2001US-0270357P.
PR 10-OCT-2001; 2001US-00974366.
PR 18-DEC-2001; 2001US-00022066.
XX
PA (HILD/) HILDEBRAND W H.
PA (PRIL/) PRILLIMAN K R.
PA (HICK/) HICKMAN H D.
XX
PI Hildebrand WH, Prilliman KR, Hickman HD;
XX
DR WPI, 2002-732755/79.
XX
XX

PT Human leukocyte antigen ligand database assembled by producing HLA having
XX loaded ligands, isolating and sequencing loaded ligands to obtain HLA
XX ligand data and populating database in computer system with ligand data.
XX
XX Disclosure; Fig 5; 118pp; English.

PS The present invention describes a human leukocyte antigen (HLA) (e.g.
XX soluble HLA) ligand database assembled by a process which involves
XX providing a computer system capable of storing HLA data as a database,
XX producing HLA having ligands loaded on it, isolating the loaded ligands
XX from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
XX populating the database with HLA ligand data. Also described: (1)
XX accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
XX system for HLA (e.g. sHLA) ligand database. The database is populated
XX with HLA ligand sequences, motifs, extended motifs, submotifs, ligands

CC unique to infected cells, tumour specific ligands, as well as a
CC collection of current and future developed HLA ligand sequences. The
CC database which contains endogenously bound and loaded ligands facilitates
CC searching of viral, bacterial, tumour or human protein sequences for
CC ligands likely to bind a particular HLA class I or class II protein. The
CC database allows the user to screen an unknown peptide sequence for
CC potential matches with sHLA ligand discrete sequences or sHLA ligand
CC motifs of sequences. Due to the completeness and concentration of sHLA
CC obtained to date, better sequencing data of numerous endogenously loaded
CC HLA ligands is found in the sHLA ligand database, and by comparison of
CC such ligands to each other and to the genomic sequence, better motifs are
CC also found in the sHLA ligand database. ABP5592 to ABP5912 represent
XX amino acid sequences used in the exemplification of the present invention
XX
SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| | |
2 GAY 4

Db

RESULT 6
ABP55796
ID ABP55796 standard; peptide; 4 AA.
XX
AC ABP55796;
XX
DT 25-FEB-2003 (first entry)
XX
DE B15 class I sHLA molecule ligand related peptide #90.
XX
KW HLA ligand; human leukocyte antigen; predictive algorithm; database;
KM MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
XX
OS Synthetic.
XX
PN WO200269198-A2.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005298.
XX
PR 21-FEB-2001; 2001US-0270357P.
PR 10-OCT-2001; 2001US-00974366.
PR 18-DEC-2001; 2001US-00022066.
XX
PA (HILD/) HILDEBRAND W H.
PA (PRIL/) PRILLIMAN K R.
PA (HICK/) HICKMAN H D.
XX
PI Hildebrand WH, Prilliman KR, Hickman HD;
XX
DR WPI, 2002-732755/79.
XX
XX

PT Human leukocyte antigen ligand database assembled by producing HLA having
XX loaded ligands, isolating and sequencing loaded ligands to obtain HLA
XX ligand data and populating database in computer system with ligand data.
XX
XX Disclosure; Fig 5; 118pp; English.

PS The present invention describes a human leukocyte antigen (HLA) (e.g.
XX soluble HLA) ligand database assembled by a process which involves
XX providing a computer system capable of storing HLA data as a database,
XX producing HLA having ligands loaded on it, isolating the loaded ligands
XX from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
XX populating the database with HLA ligand data. Also described: (1)
XX accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
XX system for HLA (e.g. sHLA) ligand database. The database is populated
XX with HLA ligand sequences, motifs, extended motifs, submotifs, ligands

CC unique to infected cells, tumour specific ligands, as well as a
 CC collection of current and future developed HLA ligand sequences. The
 CC database which contains endogenously bound and loaded ligands facilitates
 CC searching of viral, bacterial, tumour or human protein sequences for
 CC ligands likely to bind a particular HLA class I or class II protein. The
 CC database allows the user to screen an unknown peptide sequence for
 CC potential matches with SHLA ligand discrete sequences or SHLA ligand
 CC motifs of sequences. Due to the completeness and concentration of SHLA
 CC obtained to date, better sequencing data of numerous endogenously loaded
 CC HLA ligands is found in the SHLA ligand database, and by comparison of
 CC such ligands to each other and to the genomic sequence, better motifs are
 CC also found in the SHLA ligand database. AB955692 to AB955912 represent
 CC amino acid sequences used in the exemplification of the present invention
 SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 2 GAY 4

RESULT 7
 ABG96845 ID ABG96845 standard; peptide; 4 AA.

AC ABG96845;

DT 16-DEC-2002 (first entry)

DE Human leukocyte antigen (HLA) B15 ligand #170.

KW Soluble human leukocyte antigen; HLA; SHLA; cell pharm;
 KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
 KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
 KW major histocompatibility complex; diagnostic development;
 KW HLA class I polymorphism; HLA-B15 allotype; ligand.

OS Homo sapiens.

PN WO200262846-A2.

PD 15-AUG-2002.

PE 18-DEC-2001; 2001WO-US049744.

PR 18-DEC-2000; 2000US-0256409P.

PR 18-DEC-2000; 2000US-0256410P.

PR 10-OCT-2001; 2001US-00974366.

PA (HILD/) HILDEBRAND W H.

PA (PRIL/) PRILLIMAN K R.

PI Hildebrand WH, Prilliman KR;

DR WPI; 2002-698563/75.

PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
 PT studies of peptide loading for characterizing human immune responses
 PT involves using HLA allelic CDNA or genomic DNA as starting material.
 XX
 XX
 PS Disclosure; Page 178; 300pp; English.

CC The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules (SHLA) in cell pharm involving amplifying HLA
 CC allelic DNA by PCR using a locus specific primer to produce truncated a
 CC PCR product (PI), inserting PI into mammalian expression vector,
 CC electroporating the plasmid into a host cell, inoculating the cell pharm
 CC with the host cell such that cell pharm produces SHLA. A multimeric HLA
 CC complex (I) is useful for testing functionality of peptide ligands bound

CC by at least two soluble HLA molecules. (I) can be tested for its ability
 CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
 CC responses in humans. (I) is useful for studying T cell responses to
 CC pathological conditions such as viral infections and cancer, and for
 CC modulating the human immune system to induce tolerance in autoimmune
 CC diseases. The individual secreted major histocompatibility complex (MHC)
 CC molecules produced are useful for studies of peptide loading (i.e., in
 CC vaccine development) and to the development of diagnostics. With the
 CC secreted MHC molecules, naturally loaded peptides can be eluted from the
 CC MHC molecule and characterized. The secreted MHC molecules allow the
 CC assessment of structural and functional impact of HLA class I
 CC polymorphism. The molecules are also useful to generate ligands and hence
 CC ligand maps from the peptide pools extracted from series of distinct yet
 CC related class I HLA-B15 allotypes; compare the different ligand maps to
 CC identify potentially shared elements; and characterize the elements
 CC identified to positively or negatively validate the occurrence of
 CC overlapping ligands. The truncated version of (MHC) can be produced in
 CC mammalian or insect/bacterial cells such that milligram or greater
 CC quantities of an individual class I or class II molecule can be obtained.
 CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
 SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 DB 2 GAY 4

RESULT 8
 ABG97024 ID ABG97024 standard; peptide; 4 AA.

AC ABG97024;

DT 16-DEC-2002 (first entry)

DE Human leukocyte antigen (HLA) B15 ligand #352.

KW Soluble human leukocyte antigen; HLA; SHLA; cell pharm;
 KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
 KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
 KW major histocompatibility complex; diagnostic development;
 KW HLA class I polymorphism; HLA-B15 allotype; ligand.

OS Homo sapiens.

PN WO200262846-A2.

PD 15-AUG-2002.

PE 18-DEC-2001; 2001WO-US049744.

PR 18-DEC-2000; 2000US-0256409P.

PR 18-DEC-2000; 2000US-0256410P.

PR 10-OCT-2001; 2001US-00974366.

PA (HILD/) HILDEBRAND W H.

PA (PRIL/) PRILLIMAN K R.

PI Hildebrand WH, Prilliman KR;

DR WPI; 2002-698563/75.

PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
 PT studies of peptide loading for characterizing human immune responses
 PT involves using HLA allelic CDNA or genomic DNA as starting material.
 XX
 XX
 PS Disclosure; Page 183; 300pp; English.

CC The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules (SHLA) in cell pharm involving amplifying HLA
 CC allelic DNA by PCR using a locus specific primer to produce truncated a
 CC PCR product (PI), inserting PI into mammalian expression vector;
 CC electroporating the plasmid into a host cell; inoculating the cell pharm
 CC with the host cell such that cell pharm produces SHLA. A multimeric HLA
 CC complex (I) is useful for testing functionality of peptide ligands bound
 CC by at least two soluble HLA molecules. (I) can be tested for its ability
 CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
 CC responses in humans. (I) is useful for studying T cell responses to
 CC pathological conditions such as viral infections and cancer, and for
 CC modulating the human immune system to induce tolerance in autoimmune
 CC diseases. The individual secreted major histocompatibility complex (MHC)
 CC molecules produced are useful for studies of peptide loading (i.e., in
 CC vaccine development) and to the development of diagnostics. With the
 CC secreted MHC molecules, naturally loaded peptides can be eluted from the
 CC MHC molecule and characterized. The secreted MHC molecules allow the
 CC assessment of structural and functional impact of HLA class I
 CC polymorphism. The molecules are also useful to generate ligands and hence
 CC ligand maps from the peptide pools extracted from series of distinct yet
 CC related class I HLA-B*15 allotypes; compare the different ligand maps to
 CC identify potentially shared elements; and characterize the elements
 CC identified to positively or negatively validate the occurrence of
 CC overlapping ligands. The truncated version of (MHC) can be produced in
 CC mammalian or insect/bacterial cells such that milligram or greater
 CC quantities of an individual class I or class II molecule can be obtained.
 CC This sequence represents a HLA (human leukocyte antigen) peptide ligand

XX Sequence 4 AA;

Query Match: 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 2 GAY 4

DB

RESULT 9

ABG96697 standard; peptide; 4 AA.

XX ABG96697;

DT 16-DEC-2002 (first entry)

DE Human leukocyte antigen (HLA) B15 ligand #120.

KM Soluble human leukocyte antigen; HLA; SHLA; cell pharm;
 KM multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
 KM viral infection; cancer; autoimmune disease; vaccine development; MHC;
 KM major histocompatibility complex; diagnostic development;
 KM HLA class I polymorphism; HLA-B*15 allotype; ligand.

OS Homo sapiens.

PN WO200262846-A2.

PD 15-AUG-2002.

PE 16-DEC-2001; 2001WO-US049744.

PR 16-DEC-2000; 2000US-0256409P.

PR 18-DEC-2000; 2000US-0256410P.

PR 10-OCT-2001; 2001US-00974366.

PA (HILB) HILDEBRAND W. H.

PA (PRIL) PRILLMAN K. R.

PI Hildebrand WH, Prillman KR;
 DR WPI; 2002-698563/75.

XX Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
 PT studies of peptide loading for characterizing human immune responses
 PT involves using HLA allelic cDNA or genomic DNA as starting material.
 XX Disclosure; Fig 26; 300pp; English.

CC The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules (SHLA) in cell pharm involving amplifying HLA
 CC allelic DNA by PCR using a locus specific primer to produce truncated a
 CC PCR product (PI), inserting PI into mammalian expression vector;
 CC electroporating the plasmid into a host cell; inoculating the cell pharm
 CC with the host cell such that cell pharm produces SHLA. A multimeric HLA
 CC complex (I) is useful for testing functionality of peptide ligands bound
 CC by at least two soluble HLA molecules. (I) can be tested for its ability
 CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
 CC responses in humans. (I) is useful for studying T cell responses to
 CC pathological conditions such as viral infections and cancer, and for
 CC modulating the human immune system to induce tolerance in autoimmune
 CC diseases. The individual secreted major histocompatibility complex (MHC)
 CC molecules produced are useful for studies of peptide loading (i.e., in
 CC vaccine development) and to the development of diagnostics. With the
 CC secreted MHC molecules, naturally loaded peptides can be eluted from the
 CC MHC molecule and characterized. The secreted MHC molecules allow the
 CC assessment of structural and functional impact of HLA class I
 CC polymorphism. The molecules are also useful to generate ligands and hence
 CC ligand maps from the peptide pools extracted from series of distinct yet
 CC related class I HLA-B*15 allotypes; compare the different ligand maps to
 CC identify potentially shared elements; and characterize the elements
 CC identified to positively or negatively validate the occurrence of
 CC overlapping ligands. The truncated version of (MHC) can be produced in
 CC mammalian or insect/bacterial cells such that milligram or greater
 CC quantities of an individual class I or class II molecule can be obtained.
 CC This sequence represents a HLA (human leukocyte antigen) peptide ligand

XX Sequence 4 AA;

Query Match: 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 2 GAY 4

DB

RESULT 10

ABP67652 standard; peptide; 4 AA.

XX ABP67652;

DT 10-DEC-2002 (first entry)

DE Human CD66 family modulating peptide SEQ ID NO 523.

KM Human; CD66; CEACAM; cytostatic; antiinflammatory; immunomodulator;
 KM antibacterial; virucide; gene therapy; vaccine; neutrophil;
 KM immune system; autoimmune disease; cancer; infection; bacterial; virus;
 KM inflammatory disease; transplantation; immunisation.

OS Homo sapiens.

PN WO200268601-A2.

PD 06-SEP-2002.

PE 27-FEB-2002; 2002WO-US005720.

PR 28-FEB-2001; 2001US-0272113P.

PA (SKUB) SKUBITZ K M.

PA (SKUB) SKUBITZ A P N.

XX Skubitz KM, Skubitz APN;
 PS Claim 2, Page 30; 96pp; English.
 XX WPI, 2002-706981/76.
 DR New peptide from a surface exposed region of a CD66 family member, useful
 XX for modulating the function of CD66 family members, e.g. activation of
 PT neutrophils, for treating or diagnosing autoimmune diseases or cancer,
 PT and as a vaccine.
 PS Claim 2, Page 30; 96pp; English.
 XX The invention relates to an isolated peptide (1) from a surface exposed
 CC region of a CD66 family member (ABP67130-ABP67990). The peptide
 CC modulates: (a) activation of neutrophils; (b) activation or inhibition of
 CC T-cells, B-cells, NK cells, LAK cells, dendritic cells or other immune
 CC system cells; (c) proliferation and/or differentiation of the above
 CC cells, including epithelial cells; (d) homotypic and/or heterotypic
 CC adhesion among CD66 family members; and (e) adhesion of CD66 family
 CC members to other ligands. The peptide is useful in modulating the
 CC function of CD66 family members and/or their ligands, such as activation
 CC of neutrophils and activation, inhibition, proliferation and/or
 CC differentiation of the immune cells. The peptides may also be used in
 CC treating or diagnosing autoimmune diseases, cancer, infections (e.g.
 CC bacterial or viral) or inflammatory diseases, in transplantation
 CC therapies and for immunisation
 CC
 SQ Sequence 4 AA;
 Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 Db 2 GSY 4
 RESULT 11
 ABP67653
 ID ABP67653 standard; peptide; 4 AA.
 XX
 AC ABP67653;
 XX
 DT 10-DEC-2002 (first entry)
 XX
 DE Human CD66 family modulating peptide SEQ ID NO 524.
 XX
 DE Human; CD66; CEACAM; cytostatic; anti-inflammatory; immunomodulator;
 KM antibacterial; virucide; gene therapy; vaccine; neutrophil;
 KM immune system; autoimmune disease; cancer; infection; bacterial; virus;
 KM inflammatory disease; transplantation; immunisation.
 XX
 OS Homo sapiens.
 XX
 PN WO200268601-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 27-FEB-2002; 2002WO-US005720.
 XX
 PR 28-FEB-2001; 2001US-0272113P.
 XX
 PA (SKUBITZ K M.
 XX (SKUBITZ A P N.
 PA (SKUBITZ A P N.
 PI Skubitz KM, Skubitz APN;
 XX
 DR WPI, 2002-706981/76.
 XX
 PT New peptide from a surface exposed region of a CD66 family member, useful
 PT for modulating the function of CD66 family members, e.g. activation of
 PT neutrophils, for treating or diagnosing autoimmune diseases or cancer,

PT and as a vaccine.
 XX
 PS Claim 2, Page 30; 96pp; English.
 XX WPI, 2002-706981/76.
 DR New peptide from a surface exposed region of a CD66 family member, useful
 XX for modulating the function of CD66 family members, e.g. activation of
 PT neutrophils, for treating or diagnosing autoimmune diseases or cancer,
 PT and as a vaccine.
 PS Claim 2, Page 30; 96pp; English.
 XX The invention relates to an isolated peptide (1) from a surface exposed
 CC region of a CD66 family member (ABP67130-ABP67990). The peptide
 CC modulates: (a) activation of neutrophils; (b) activation or inhibition of
 CC T-cells, B-cells, NK cells, LAK cells, dendritic cells or other immune
 CC system cells; (c) proliferation and/or differentiation of the above
 CC cells, including epithelial cells; (d) homotypic and/or heterotypic
 CC adhesion among CD66 family members; and (e) adhesion of CD66 family
 CC members to other ligands. The peptide is useful in modulating the
 CC function of CD66 family members and/or their ligands, such as activation
 CC of neutrophils and activation, inhibition, proliferation and/or
 CC differentiation of the immune cells. The peptides may also be used in
 CC treating or diagnosing autoimmune diseases, cancer, infections (e.g.
 CC bacterial or viral) or inflammatory diseases, in transplantation
 CC therapies and for immunisation
 CC
 SQ Sequence 4 AA;
 Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 Db 1 GSY 3
 RESULT 12
 AAU84247
 ID AAU84247 standard; peptide; 4 AA.
 XX
 AC AAU84247;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Caspase cleavage site #11.
 XX
 DE Caspase; apoptosis; GAP SH3 binding protein; HCD2; AOP-1; cancer;
 KM apoptotic-associated disease; hyperproliferative disease; AIDS;
 KM degenerative disease; autoimmune disease; Alzheimer's disease;
 KM viral infection; acquired immunodeficiency syndrome; vascular disease;
 KM myocardial infarction; oxidative stress; ischemic stroke; arthritis;
 KM heart failure; Parkinson's disease; amyotrophic lateral sclerosis.
 XX
 OS Unidentified.
 XX
 PN WO200196673-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 15-JUN-2001; 2001WO-EP006780.
 XX
 PR 16-JUN-2000; 2000EP-00112813.
 XX 16-NOV-2000; 2000EP-00125013.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Rudel T, Thiede B, Machuy N;
 XX
 DR WPI, 2002-098088/13.
 XX
 PT Novel apoptosis-associated and/or -modified protein useful as target for
 PT the diagnosis, prevention or treatment of apoptosis-associated diseases
 PT particularly neurodegenerative diseases.
 XX
 PS Claim 30; Page 62; 86pp; English.
 XX
 CC The invention relates to an apoptosis-associated and/or -modified protein
 CC (1) selected from GAP SH3 binding protein, HCD2 and AOP-1 (not defined)
 CC or its proteolytic fragments. (1) is useful as target for the diagnosis,

CC prevention or treatment of apoptosis-associated diseases, for the
 CC manufacture of a pharmaceutical agent and for identifying apoptosis
 CC modulators. The proteome is useful as a target for the diagnosis,
 CC prevention or treatment of apoptosis-associated diseases, and in a method
 CC for identifying apoptosis modulators. (i) is useful for treatment of
 CC hyperproliferative or degenerative diseases including cancers, autoimmune
 CC diseases, Alzheimer's disease, viral infections such as acquired
 CC immunodeficiency syndrome (AIDS) and vascular diseases such as myocardial
 CC infection. (i) is also useful for treating and/or preventing diseases
 CC related to oxidative stress like ischemic stroke, arthritis, heart
 CC failure, Parkinson's disease and amyotrophic lateral sclerosis. (i) is
 CC also useful for developing protein chips or other solid phase screening
 CC devices for high throughput screens, and also as a diagnostic tool to
 CC screen for caspase activity, and/or to determine the effectivity of
 CC caspase cleavage inhibiting and/or modulating substances. AA084237-
 CC AA084260 represent caspase cleavage sites of the invention
 CC
 SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 DB 1 GSY 3

RESULT 13
 AB018638
 ID AB018638 standard; peptide; 4 AA.
 AC AB018638;
 XX
 DT 20-FEB-2003 (first entry)
 XX
 DE ErbB receptor antagonist peptide #21.
 XX
 KM Vaccine; erbB receptor antagonist; tumour; cancer; gastric cancer;
 KM breast cancer; prostate cancer.
 OS Unidentified.
 XX
 PN WO200281649-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 08-APR-2002; 2002WO-US011211.
 XX
 PR 06-APR-2001; 2001US-0282037P.
 PR 03-AUG-2001; 2001US-0309864P.
 XX
 PA (TYPE-) UNIV PENNSYLVANIA.
 XX
 PI Greene MI, Zhang H, Murali R, Richter M, Berezov A, Liu Q,
 PI Chen J;
 XX
 DR WPI; 2003-075482/07.
 XX
 PT New peptide antagonists against erbB receptors, useful for preventing or
 PT treating tumors or cancers (e.g. lung adenocarcinomas, breast carcinomas
 PT or prostate cancer) in humans;
 XX
 PS Claim 1; Page 82; 115pp; English.
 XX
 CC The invention comprises peptide antagonists designed to target erbB
 CC receptors. The erbB receptor peptide antagonists are useful for
 CC preventing tumors and cancers (e.g. gastric cancer, breast cancer and
 CC prostate cancer). The present amino acid sequence represents an erbB
 CC receptor peptide antagonist of the invention
 XX
 SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 6; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 DB 2 GSY 4

RESULT 14
 ABP59243
 ID ABP59243 standard; peptide; 4 AA.
 AC ABP59243;
 XX
 DT 10-MAY-2003 (first entry)
 XX
 DE Peptide epitope for generating cell surface receptor antibody, SEQ ID 21.
 XX
 KM Antibody; cytostatic; vaccine; cell surface receptor; erbB; TNF;
 KM immunoglobulin gene superfamily; IGSF; epitope.
 OS Synthetic.
 XX
 PN WO2003012072-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 05-AUG-2002; 2002WO-US024892.
 XX
 PR 03-AUG-2001; 2001US-0309864P.
 XX
 PA (TYPE-) UNIV PENNSYLVANIA.
 XX
 PI Greene MI, Zhang H, Richter M, Murali R;
 PI WPI; 2003-268117/26.
 XX
 DR
 XX

PT Novel antibody for preventing, treating, imaging or diagnosing tumor, has
 PT specificity for activated cell surface receptor and binds specifically to
 PT an epitope that does not comprise phosphotyrosine residue.
 XX

PS Claim 53; Page 88; 114pp; English.

CC The present invention relates to novel antibodies, which have specificity
 CC for activated cell surface receptors (erbB, TNF and immunoglobulin gene
 CC superfamily; IGSF) and bind to an epitope (ABP59223-ABP59259). The
 CC antibodies are useful for preventing transformation of a normal cell into
 CC a tumour cell in a patient who had a tumour with tumour cells that
 CC express activated erbB receptors on the cell surface surgically removed
 CC or in whom the tumour has entered remission, for treating a patient
 CC suffering from a cancer characterised by tumour cells that have p185 on
 CC their cell surfaces, or for treating a patient suffering from an erbB
 CC tumour. The antibodies were produced by immunising a suitable host with a
 CC peptide (ABP59223-ABP59259), or its reverse sequence
 XX

SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 6; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 DB 2 GSY 4

RESULT 15
 AD081984
 ID AD081984 standard; peptide; 4 AA.
 AC AD081984;
 XX

XX 06-MAY-2004 (first entry)
 DT Thermus brockianus nucleic acid polymerase peptide fragment #2.
 XX
 DE nucleic acid polymerase; thermophile; mutation; exonuclease activity.
 XX
 KW Thermus brockianus.
 OS
 XX WO2003048308-A2.
 PN
 XX 12-JUN-2003.
 PD
 XX
 PF 22-NOV-2002; 2002WO-US037657.
 XX
 PR 30-NOV-2001; 2001US-0334434P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Rozzelle J, Bolchakova E;
 XX
 DR WPI; 2003-505285/47.
 XX
 PT New Thermus brockianus nucleic acid polymerases, useful for DNA
 PT synthesis, primer extension, DNA sequencing, reverse transcription, or
 PT DNA and RNA amplification procedures.
 XX
 PS Disclosure; SEQ ID NO 18; 74pp; English.
 XX
 CC The invention relates to novel nucleic acid polymerases from the
 CC thermophilic organism Thermus brockianus or mutants having a mutation
 CC that decreases 5'-3' exonuclease activity or reduces discrimination
 CC against diideoxynucleotide triphosphates. The nucleic acid polymerases,
 CC isolated nucleic acids encoding the polymerases, vectors, host cells and
 CC kits are useful for DNA synthesis, primer extension, DNA sequencing,
 CC reverse transcription, or DNA and RNA amplification procedures. The
 CC nucleic acids are also useful for the recombinant expression of the
 CC polymerase polypeptides. The nucleic acid polymerases and nucleic acids
 CC are useful for the detection and isolation of nucleic acids encoding DNA
 CC polymerase I activity. This sequence corresponds to a peptide of a
 CC polymerase of the invention.
 CC
 SQ Sequence 4 AA;
 QY
 QY 1 GAY 3 86.7%; Score 13; DB 7; Length 4;
 DB 1 GAY 3 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: December 13, 2004, 22:22:40
 Job time : 81 secs

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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:12:37 (Search time 21.4 seconds
(without alignments)
12.396 Million cell updates/sec

Title: US-10-068-905-7

Perfect score: 15

Sequence: 1 GXYX 4

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	86.7	4	1	US-08-798-897-49 Sequence 49, Appl
2	13	86.7	4	1	US-08-463-224-2 Sequence 2, Appl
3	13	86.7	4	2	US-08-463-377-2 Sequence 2, Appl
4	13	86.7	4	2	US-08-978-523-49 Sequence 49, Appl
5	13	86.7	4	2	US-08-310-912A-199 Sequence 199, Appl
6	13	86.7	4	3	US-09-301-085-199 Sequence 199, Appl
7	13	86.7	4	5	PCT-US83-01668-41 Sequence 41, Appl
8	13	86.7	4	5	PCT-US93-04589-199 Sequence 199, Appl
9	13	86.7	5	1	US-07-962-569A-6 Sequence 6, Appl
10	13	86.7	5	1	US-08-292-968-30 Sequence 36, Appl
11	13	86.7	5	2	US-08-618-696-3 Sequence 36, Appl
12	13	86.7	5	2	US-08-618-696-3 Sequence 14, Appl
13	13	86.7	5	2	US-08-467-874-30 Sequence 30, Appl
14	13	86.7	5	2	US-08-467-874-30 Sequence 36, Appl
15	13	86.7	5	2	US-08-467-874-30 Sequence 36, Appl
16	13	86.7	5	2	US-08-467-874-30 Sequence 36, Appl
17	13	86.7	5	2	US-08-467-874-30 Sequence 36, Appl
18	13	86.7	5	3	US-09-033-753-3 Sequence 36, Appl
19	13	86.7	5	3	US-09-033-753-3 Sequence 14, Appl
20	13	86.7	5	3	US-08-467-874-30 Sequence 36, Appl
21	13	86.7	5	3	US-08-467-874-30 Sequence 36, Appl
22	13	86.7	5	3	US-09-082-514-30 Sequence 30, Appl
23	13	86.7	5	3	US-09-082-514-30 Sequence 36, Appl
24	13	86.7	5	4	US-08-475-955-143 Sequence 143, Appl
25	13	86.7	6	1	US-08-014-979-92 Sequence 92, Appl
26	13	86.7	6	1	US-08-176-620A-21 Sequence 21, Appl
27	13	86.7	6	1	US-08-248-538-20 Sequence 20, Appl

28	13	86.7	6	1	US-08-248-538-40 Sequence 40, Appl
29	13	86.7	6	1	US-08-260-199A-31 Sequence 31, Appl
30	13	86.7	6	1	US-08-260-199A-32 Sequence 32, Appl
31	13	86.7	6	1	US-08-798-897-53 Sequence 53, Appl
32	13	86.7	6	1	US-08-690-605-21 Sequence 21, Appl
33	13	86.7	6	2	US-08-580-988A-16 Sequence 16, Appl
34	13	86.7	6	2	US-08-461-985-21 Sequence 21, Appl
35	13	86.7	6	2	US-08-978-523-53 Sequence 53, Appl
36	13	86.7	6	3	US-08-481-985B-132 Sequence 132, Appl
37	13	86.7	6	3	US-08-932-787B-12 Sequence 12, Appl
38	13	86.7	6	3	US-08-932-012C-12 Sequence 12, Appl
39	13	86.7	6	3	US-08-888-818C-12 Sequence 12, Appl
40	13	86.7	6	4	US-09-518-737-6 Patent No. 5200320
41	13	86.7	6	4	US-09-518-737-6 Patent No. 5200320
42	13	86.7	7	1	US-07-841-997A-19 Sequence 19, Appl
43	13	86.7	7	1	US-08-290-301-19 Sequence 19, Appl
44	13	86.7	7	2	US-09-070-786-8 Sequence 8, Appl
45	13	86.7	7	3	US-09-193-104-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-798-897-49
Sequence 49, Application US/08798897
Patent No. 5789201

GENERAL INFORMATION:

APPLICANT: Gaestrella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:

28	13	86.7	6	1	US-08-248-538-40 Sequence 40, Appl
29	13	86.7	6	1	US-08-260-199A-31 Sequence 31, Appl
30	13	86.7	6	1	US-08-260-199A-32 Sequence 32, Appl
31	13	86.7	6	1	US-08-798-897-53 Sequence 53, Appl
32	13	86.7	6	1	US-08-690-605-21 Sequence 21, Appl
33	13	86.7	6	2	US-08-580-988A-16 Sequence 16, Appl
34	13	86.7	6	2	US-08-461-985-21 Sequence 21, Appl
35	13	86.7	6	2	US-08-978-523-53 Sequence 53, Appl
36	13	86.7	6	3	US-08-481-985B-132 Sequence 132, Appl
37	13	86.7	6	3	US-08-932-787B-12 Sequence 12, Appl
38	13	86.7	6	3	US-08-932-012C-12 Sequence 12, Appl
39	13	86.7	6	3	US-08-888-818C-12 Sequence 12, Appl
40	13	86.7	6	4	US-09-518-737-6 Patent No. 5200320
41	13	86.7	6	4	US-09-518-737-6 Patent No. 5200320
42	13	86.7	7	1	US-07-841-997A-19 Sequence 19, Appl
43	13	86.7	7	1	US-08-290-301-19 Sequence 19, Appl
44	13	86.7	7	2	US-09-070-786-8 Sequence 8, Appl
45	13	86.7	7	3	US-09-193-104-28 Sequence 28, Appl

US-08-798-897-49

Query Match 86.7% Score 13; DB 1; Length 4;

Best Local Similarity 66.7% Pred. No. 3.8e+05; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 1;

QY 1 GXY 3

DB 2 GAY 4

RESULT 2
US-08-463-224-2
Sequence 2, Application US/08463224
Patent No. 5807824
GENERAL INFORMATION:
APPLICANT: van Oostrum, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
Substantially No. 5807824 Agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,224
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-224-2
Query Match
Best Local Similarity 86.7%; Score 13; DB 1; Length 4;
Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GAY 4

RESULT 3
US-08-463-377-2
Sequence 2, Application US/08463377
Patent No. 5837499
GENERAL INFORMATION:
APPLICANT: van Oostrum, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
Substantially No. 5837499 Agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,377
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-377-2
Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 4;
Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GAY 4

RESULT 4
US-08-978-523-49
Sequence 49, Application US/08978523
Patent No. 5883225
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
-TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-978-523-49

Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
1
2 GAY 4

RESULT 5
US-08-310-912A-199

Sequence 199, Application US/08310912A
Patent No. 5981730
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,912A
FILING DATE: September 22, 1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/227,360
FILING DATE: April 13, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/254001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-310-912A-199

Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
1
2 GTY 4

RESULT 6
US-09-301-085-199

Sequence 199, Application US/09301085
Patent No. 6262248
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
TITLE OF INVENTION: DETECTION METHODS
FILE REFERENCE: 00786/254002
CURRENT APPLICATION NUMBER: US/09/301,085
CURRENT FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: 08/310,912
EARLIER FILING DATE: 1994-09-22
EARLIER APPLICATION NUMBER: 08/227,360
EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 199
LENGTH: 4
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-301-085-199

Query Match 86.7%; Score 13; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
1
2 GTY 4

RESULT 7
PCT-US93-01669-41
Sequence 41, Application PC/TUS9301669
GENERAL INFORMATION:
APPLICANT: Trowbridge, Ian S.
APPLICANT: Collawn, Jr., James F.
APPLICANT: Tainer, John A.
APPLICANT: Kuhn, Leslie A.
TITLE OF INVENTION: RECEPTOR INTERNALIZATION SIGNALS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Judas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01669
FILING DATE: 01-MAR-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/844,852
FILING DATE: 03-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weatherell, Jr. Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1636
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-01669-41

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 8

PCT-US95-04589-199
Sequence 199, Application PC/TUS9504589
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumitaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04589
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04589-199

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 9

US-07-962-569A-6
Sequence 6, Application US/07962569A
Patent No. 5391497
GENERAL INFORMATION:
APPLICANT: MENON, RAVI S.
APPLICANT: JEFFERS, KATHLEEN F.
APPLICANT: CHANG, YING-PON
APPLICANT: HAM, RICHARD G.
TITLE OF INVENTION: HUMAN K-CASEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FREDERICK W. PEPPER, PH.D.
STREET: 11545 W. BERNARDO COURT, STE. 302
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92127
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/962,569A
FILING DATE: 19921013
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 920224.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 451-1120
TELEFAX: (619) 451-9628
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-962-569A-6

Query Match 86.7%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GTY 5

RESULT 10

US-08-292-968-30
Sequence 30, Application US/08292968
Patent No. 5856122
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COHEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARKSTRONG, Glen D.
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney

STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-388
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-968-30

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 11
US-08-292-968-36
Sequence 36, Application US/08292968
Patent No. 5856122
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COOMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KUBIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-388
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-968-36

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 12
US-08-618-696-3
Sequence 3, Application US/08618696
Patent No. 5861475
GENERAL INFORMATION:
APPLICANT: COOPER, Jr., J. ALLEN D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
INHIBITION OF PHAGOCYTES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,696
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,265
FILING DATE: 12/21/92
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UOAB:002/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acid residues
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-618-696-3

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 1 GAY 3

RESULT 13
US-08-618-696-14
Sequence 14, Application US/08618696
Patent No. 5861475

GENERAL INFORMATION:
APPLICANT: COOPER, Jr., J. ALLEN D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618, 696
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,269
FILING DATE: 12/21/92

ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UOAB:002/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-618-696-14

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 1 GAY 3

RESULT 14
US-08-467-974-30
Sequence 30, Application US/08467974
Patent No. 5965385

GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.

APPLICANT: OOMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,974
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-454 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-467-974-30

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 15
US-08-467-974-36
Sequence 36, Application US/08467974
Patent No. 5965385

GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: OOMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sim & McBurney
;; STREET: Suite 701, 330 University Avenue
;; CITY: Toronto
;; STATE: Ontario
;; COUNTRY: Canada
;; ZIP: M5G 1R7
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/467,974
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/467,536
;; FILING DATE: 06-JUN-1995
;; APPLICATION NUMBER: US 08/292,968
;; FILING DATE: 22-AUG-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/251,121
;; FILING DATE: 31-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/110,947
;; FILING DATE: 24-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEWART, Michael I.
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-454 MIS:V9
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 36:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-467-974-36

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GTY 4

Search completed: December 13, 2004, 22:34:51
Job time : 21.4 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:31:47 ; Search time 68.6 Seconds

(Without alignments)
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Title: US-10-068-905-7

Perfect score: 15

Sequence: 1 GXYY 4

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	86.7	4	9	US-09-867-852-199
2	13	86.7	4	14	US-10-302-817A-18
3	13	86.7	4	15	US-10-613-472-199
4	13	86.7	4	16	US-10-613-765-199
5	13	86.7	5	10	US-09-792-686A-34
6	13	86.7	5	14	US-10-344-779-8
7	13	86.7	5	14	US-10-346-121A-143
8	13	86.7	5	16	US-10-738-809-8
9	13	86.7	5	16	US-10-384-471B-3
10	13	86.7	5	16	US-10-384-471B-11
11	13	86.7	6	9	US-09-990-762-36
12	13	86.7	6	9	US-09-990-762-40
13	13	86.7	6	9	US-09-990-762-41

14	13	86.7	6	10	US-09-518-737-6	Sequence 6, Appli
15	13	86.7 <td>6<td>10</td><td>US-09-858-852A-36</td><td>Sequence 36, Appli</td></td>	6 <td>10</td> <td>US-09-858-852A-36</td> <td>Sequence 36, Appli</td>	10	US-09-858-852A-36	Sequence 36, Appli
16	13	86.7 <td>6<td>10</td><td>US-09-858-852A-40</td><td>Sequence 40, Appli</td></td>	6 <td>10</td> <td>US-09-858-852A-40</td> <td>Sequence 40, Appli</td>	10	US-09-858-852A-40	Sequence 40, Appli
17	13	86.7 <td>6<td>10</td><td>US-09-858-852A-41</td><td>Sequence 41, Appli</td></td>	6 <td>10</td> <td>US-09-858-852A-41</td> <td>Sequence 41, Appli</td>	10	US-09-858-852A-41	Sequence 41, Appli
18	13	86.7 <td>6<td>14</td><td>US-10-285-045-23</td><td>Sequence 23, Appli</td></td>	6 <td>14</td> <td>US-10-285-045-23</td> <td>Sequence 23, Appli</td>	14	US-10-285-045-23	Sequence 23, Appli
19	13	86.7 <td>6<td>14</td><td>US-10-284-660-23</td><td>Sequence 23, Appli</td></td>	6 <td>14</td> <td>US-10-284-660-23</td> <td>Sequence 23, Appli</td>	14	US-10-284-660-23	Sequence 23, Appli
20	13	86.7 <td>6<td>15</td><td>US-10-394-980-232</td><td>Sequence 232, Appli</td></td>	6 <td>15</td> <td>US-10-394-980-232</td> <td>Sequence 232, Appli</td>	15	US-10-394-980-232	Sequence 232, Appli
21	13	86.7 <td>6<td>15</td><td>US-10-306-631-63</td><td>Sequence 63, Appli</td></td>	6 <td>15</td> <td>US-10-306-631-63</td> <td>Sequence 63, Appli</td>	15	US-10-306-631-63	Sequence 63, Appli
22	13	86.7 <td>6<td>15</td><td>US-10-435-751-108</td><td>Sequence 108, Appli</td></td>	6 <td>15</td> <td>US-10-435-751-108</td> <td>Sequence 108, Appli</td>	15	US-10-435-751-108	Sequence 108, Appli
23	13	86.7 <td>6<td>15</td><td>US-10-435-751-121</td><td>Sequence 121, Appli</td></td>	6 <td>15</td> <td>US-10-435-751-121</td> <td>Sequence 121, Appli</td>	15	US-10-435-751-121	Sequence 121, Appli
24	13	86.7 <td>6<td>15</td><td>US-10-133-234A-17</td><td>Sequence 17, Appli</td></td>	6 <td>15</td> <td>US-10-133-234A-17</td> <td>Sequence 17, Appli</td>	15	US-10-133-234A-17	Sequence 17, Appli
25	13	86.7 <td>6<td>15</td><td>US-10-133-234A-18</td><td>Sequence 18, Appli</td></td>	6 <td>15</td> <td>US-10-133-234A-18</td> <td>Sequence 18, Appli</td>	15	US-10-133-234A-18	Sequence 18, Appli
26	13	86.7 <td>6<td>15</td><td>US-10-133-234A-19</td><td>Sequence 19, Appli</td></td>	6 <td>15</td> <td>US-10-133-234A-19</td> <td>Sequence 19, Appli</td>	15	US-10-133-234A-19	Sequence 19, Appli
27	13	86.7 <td>6<td>15</td><td>US-10-133-234A-20</td><td>Sequence 20, Appli</td></td>	6 <td>15</td> <td>US-10-133-234A-20</td> <td>Sequence 20, Appli</td>	15	US-10-133-234A-20	Sequence 20, Appli
28	13	86.7 <td>6<td>15</td><td>US-10-133-234A-21</td><td>Sequence 21, Appli</td></td>	6 <td>15</td> <td>US-10-133-234A-21</td> <td>Sequence 21, Appli</td>	15	US-10-133-234A-21	Sequence 21, Appli
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31	13	86.7 <td>6<td>17</td><td>US-10-813-638-1446</td><td>Sequence 1446, Appli</td></td>	6 <td>17</td> <td>US-10-813-638-1446</td> <td>Sequence 1446, Appli</td>	17	US-10-813-638-1446	Sequence 1446, Appli
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33	13	86.7 <td>7</td> <td>10</td> <td>US-09-792-686A-31</td> <td>Sequence 31, Appli</td>	7	10	US-09-792-686A-31	Sequence 31, Appli
34	13	86.7 <td>7</td> <td>14</td> <td>US-10-286-457-129</td> <td>Sequence 129, Appli</td>	7	14	US-10-286-457-129	Sequence 129, Appli
35	13	86.7 <td>7</td> <td>14</td> <td>US-10-286-457-189</td> <td>Sequence 189, Appli</td>	7	14	US-10-286-457-189	Sequence 189, Appli
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37	13	86.7 <td>7</td> <td>17</td> <td>US-10-741-481-35</td> <td>Sequence 35, Appli</td>	7	17	US-10-741-481-35	Sequence 35, Appli
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ALIGNMENTS

RESULT 1
US-09-867-852-199
Sequence 199, Application US/09867852
Patent No. US20020147324A1
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew P.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumaki
APPLICANT: Kunzel, Barbara N.
APPLICANT: Mindinos, Michael N.
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
FILE REFERENCE: 00786/254002
CURRENT APPLICATION NUMBER: US/09/867,852
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,065
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 199
LENGTH: 4
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-867-852-199
Query Match 86.7%; Score 13; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
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DB 2 GTY 4

RESULT 2

US-10-302-817A-18
; Sequence 18, Application US/10302817A
; Publication No. US20030198978A1
; GENERAL INFORMATION:
; APPLICANT: KOZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768US
; CURRENT APPLICATION NUMBER: US/10/302,817A
; PRIOR FILING DATE: 2002-11-22
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Thermus brockianus
US-10-302-817A-18

Query Match 86.7%; Score 13; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
DB 1 GTY 3

RESULT 3

US-10-613-472-199
; Sequence 199, Application US/10613472
; Publication No. US20040088756A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Pumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254004
; CURRENT APPLICATION NUMBER: US/10/613,472
; PRIOR FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 09/867,852
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/301,085
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: US 08/310,912
; PRIOR FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: US 08/227,360
; PRIOR FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-472-199

Query Match 86.7%; Score 13; DB 15; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
DB 2 GTY 4

RESULT 4

US-10-613-765-199
; Sequence 199, Application US/10613765
; Publication No. US20040172673A1
; GENERAL INFORMATION:
; APPLICANT: AUSUBEL, FREDERICK M.
; APPLICANT: STASKAWICZ, BRIAN J.
; APPLICANT: KATAGIRI, PUMIAKI
; APPLICANT: KUNKEL, BARBARA N.
; APPLICANT: MINDRINOS, MICHAEL N.
; APPLICANT: YU, GUO-LIANG
; APPLICANT: BAKER, BARBARA
; APPLICANT: ELLIS, JEFFREY
; APPLICANT: SALMERON, JOHN
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254005
; CURRENT APPLICATION NUMBER: US/10/613,765
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: US 09/867,852
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/301,085
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: US 08/310,912
; PRIOR FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: US 08/227,360
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-765-199

Query Match 86.7%; Score 13; DB 16; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
DB 2 GTY 4

RESULT 5

US-09-792-686A-34
; Sequence 34, Application US/09792686A
; Publication No. US20030068645A1
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Kopecky, Stephen L.
; APPLICANT: Weyand, Cornelia M.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR EVALUATING
; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
; FILE REFERENCE: 07039-250001
; CURRENT APPLICATION NUMBER: US/09/792,686A
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-686A-34

Query Match 86.7%; Score 13; DB 10; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GTY 5

RESULT 6
US-10-344-779-8
Sequence 8, Application US/103444779
Publication No. US2003021106A1
GENERAL INFORMATION:
APPLICANT: SWEET, RAYMOND W.
APPLICANT: TORNETTA, MARK A.
APPLICANT: TRUNEH, ALEMESEGED
APPLICANT: WATTAM, TREVOR A.
TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
FILE REFERENCE: GP50033
CURRENT APPLICATION NUMBER: US/10/344,779
CURRENT FILING DATE: 2003-02-17
PRIOR APPLICATION NUMBER: PCT/US01/26161
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,524
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 60/230,639
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 5
TYPE: PRT
ORGANISM: Mus musculus
US-10-344-779-8

Query Match 86.7%; Score 13; DB 14; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 1 GTY 3

RESULT 7
US-10-376-121A-143
Sequence 143, Application US/10376121A
Publication No. US2003021654A1
GENERAL INFORMATION:
APPLICANT: HARLEY, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991

APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 143:
US-10-376-121A-143

Query Match 86.7%; Score 13; DB 14; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 1 GTY 3

RESULT 8
US-10-738-809-8
Sequence 8, Application US/10738809
Publication No. US2004017117A1
GENERAL INFORMATION:
APPLICANT: SWEET, RAYMOND W.
APPLICANT: TORNETTA, MARK A.
APPLICANT: TRUNEH, ALEMESEGED
APPLICANT: WATTAM, TREVOR A.
TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
FILE REFERENCE: GP50033
CURRENT APPLICATION NUMBER: US/10/738,809
CURRENT FILING DATE: 2003-12-17
PRIOR APPLICATION NUMBER: US/10/344,779
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: PCT/US01/26161
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,524
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 60/230,639
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 5
TYPE: PRT
ORGANISM: Mus musculus
US-10-738-809-8

Query Match 86.7%; Score 13; DB 16; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 1 GTY 3

RESULT 9
US-10-394-471B-3
Sequence 3, Application US/10394471B
Publication No. US20040185047A1
GENERAL INFORMATION:
APPLICANT: GILES-KOMAR, Jill; Carlton, Jill; Scallion, Bernard J.

;; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
;; FILE REFERENCE: CEN0202
;; CURRENT APPLICATION NUMBER: US/10/394,471B
;; CURRENT FILING DATE: 2003-03-21
;; PRIOR APPLICATION NUMBER: 60/367,903
;; PRIOR FILING DATE: 2002-03-26
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: Patentln Ver 3.1
;; SEQ ID NO 3
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-394-471B-3

Query Match 86.7%; Score 13; DB 16; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GSY 4

RESULT 10
US-10-394-471B-11
;; Sequence 11, Application US/10394471B
;; Patent No. US20040185047A1
;; GENERAL INFORMATION:
;; APPLICANT: GILES-KOMAR, JILL; CARTON, JILL; SCALLON, BERNARD J.
;; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
;; FILE REFERENCE: CEN0202
;; CURRENT APPLICATION NUMBER: US/10/394,471B
;; CURRENT FILING DATE: 2003-03-21
;; PRIOR APPLICATION NUMBER: 60/367,903
;; PRIOR FILING DATE: 2002-03-26
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: Patentln Ver 3.1
;; SEQ ID NO 11
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-394-471B-11

Query Match 86.7%; Score 13; DB 16; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GSY 4

RESULT 11
US-09-990-762-36
;; Sequence 36, Application US/09990762
;; Patent No. US20020119498A1
;; GENERAL INFORMATION:
;; APPLICANT: JOUNG, J. KEITH
;; APPLICANT: MILLER, JEFFREY
;; APPLICANT: PABO, CARL O.
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
;; FILE REFERENCE: MTV-030.02 (20021-3002)
;; CURRENT APPLICATION NUMBER: US/09/990,762
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 09/858,852
;; PRIOR FILING DATE: 2001-05-16
;; PRIOR APPLICATION NUMBER: 60/204,509
;; PRIOR FILING DATE: 2000-05-16
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 36
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
;; OTHER INFORMATION: recognition sequence
US-09-990-762-36

Query Match 86.7%; Score 13; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 3 GAY 5

RESULT 12
US-09-990-762-40
;; Sequence 40, Application US/09990762
;; Patent No. US20020119498A1
;; GENERAL INFORMATION:
;; APPLICANT: JOUNG, J. KEITH
;; APPLICANT: MILLER, JEFFREY
;; APPLICANT: PABO, CARL O.
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
;; FILE REFERENCE: MTV-030.02 (20021-3002)
;; CURRENT APPLICATION NUMBER: US/09/990,762
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 09/858,852
;; PRIOR FILING DATE: 2001-05-16
;; PRIOR APPLICATION NUMBER: 60/204,509
;; PRIOR FILING DATE: 2000-05-16
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 40
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
;; OTHER INFORMATION: recognition sequence
US-09-990-762-40

Query Match 86.7%; Score 13; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 3 GAY 5

RESULT 13
US-09-990-762-41
;; Sequence 41, Application US/09990762
;; Patent No. US20020119498A1
;; GENERAL INFORMATION:
;; APPLICANT: JOUNG, J. KEITH
;; APPLICANT: MILLER, JEFFREY
;; APPLICANT: PABO, CARL O.
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
;; FILE REFERENCE: MTV-030.02 (20021-3002)
;; CURRENT APPLICATION NUMBER: US/09/990,762
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 09/858,852
;; PRIOR FILING DATE: 2001-05-16
;; PRIOR APPLICATION NUMBER: 60/204,509
;; PRIOR FILING DATE: 2000-05-16
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 41
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
OTHER INFORMATION: recognition sequence
US-09-990-762-41

Query Match
Best Local Similarity 86.7%; Score 13; DB 9; Length 6;
Matches 2; Conservative 0; Pred. No. 1.4e+06; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GAY 5

RESULT 14
US-09-518-737-6
Sequence 6, Application US/09518737
Publication No. US20030008321A1
GENERAL INFORMATION:
APPLICANT: FUKUI, YASUHIKA
APPLICANT: NAGATA, SATOSHI
APPLICANT: SHIRAI, RYUICHI
APPLICANT: SAITO, NAOAKI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
FILE REFERENCE: 1965/49618
CURRENT APPLICATION NUMBER: US/09/518,737
CURRENT FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: JP 1999-250209
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 6
TYPE: PRT
ORGANISM: Mus musculus
US-09-518-737-6

Query Match
Best Local Similarity 86.7%; Score 13; DB 10; Length 6;
Matches 2; Conservative 0; Pred. No. 1.4e+06; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GAY 6

RESULT 15
US-09-858-852A-36
Sequence 36, Application US/09858852A
Publication No. US20030044787A1
GENERAL INFORMATION:
APPLICANT: JUNG, J. KEITH
APPLICANT: MILLER, JEFFREY
APPLICANT: PABO, CARL O.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
FILE REFERENCE: MTW-030.01 (20021-3001)
CURRENT APPLICATION NUMBER: US/09/858,852A
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/204,509
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
OTHER INFORMATION: recognition sequence
US-09-858-852A-36

Query Match 86.7%; Score 13; DB 10; Length 6;

Best Local Similarity 86.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GAY 5

Search completed: December 13, 2004, 23:02:40
Job time : 69.6 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:01:21 ; Search time 15.2 seconds

(without alignments)
25.320 Million cell updates/sec

Title: US-10-068-905-7

Perfect score: 15

Sequence: 1 GXY 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR.79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	86.7	9	2	S36850
2	13	86.7	9	2	G41946
3	13	86.7	11	2	PT0250
4	13	86.7	11	2	PT0214
5	13	86.7	12	2	A33099
6	13	86.7	12	2	S47391
7	13	86.7	12	2	S47395
8	13	86.7	12	2	PH1611
9	13	86.7	12	2	PH0802
10	13	86.7	12	2	PH0790
11	13	86.7	13	2	S47368
12	13	86.7	13	2	S47383
13	13	86.7	13	2	PH0788
14	13	86.7	13	2	A50700
15	13	86.7	14	2	A59018
16	13	86.7	14	2	PH1601
17	13	86.7	14	2	PH0792
18	13	86.7	15	2	PH1582
19	13	86.7	16	2	S11290
20	13	86.7	17	2	S48655
21	13	86.7	17	2	A60317
22	13	86.7	17	2	F35141
23	13	86.7	18	2	I73024
24	13	86.7	18	2	PH1629
25	13	86.7	19	2	PH1609
26	13	86.7	20	2	EX0059
27	13	86.7	20	2	UA0142
28	13	86.7	20	2	A54519
29	13	86.7	20	2	PE0161

30	13	86.7	20	2	S44465	pyrrolicoridin - Py
31	13	86.7	21	2	PT0227	Ig heavy chain CDR
32	13	86.7	21	2	S47198	T-cell receptor J-
33	13	86.7	21	2	S47212	T-cell receptor J-
34	13	86.7	22	2	PH1680	Ig heavy chain V x
35	13	86.7	22	2	A53794	lyticidine synthase
36	13	86.7	23	2	A53631	H+-transporting tw
37	13	86.7	23	2	PH1725	Ig heavy chain V x
38	13	86.7	24	2	I73584	alpha 1-proteinase
39	13	86.7	24	2	I61491	seed protein ws-9
40	13	86.7	24	2	D27579	T-cell receptor be
41	13	86.7	24	2	A05298	fibrinogen gamma c
42	13	86.7	24	2	E45087	cysteine proteinase
43	13	86.7	24	2	S56000	guanidino kinase M
44	13	86.7	25	2	A58647	alpha-conotoxin P
45	13	86.7	26	2	PQ0105	alkaline serine pr

ALIGNMENTS

RESULT 1

S36850

Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999

C/Accession: S36850

R/Jacob, J.; Keisoe, G.

submitted to the EMBL Data Library, July 1992

A/Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophen

A/Reference number: S25024

A/Accession: S36850

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-9 <JAC>

A/Cross-references: EMBL:X67387; NID:G50113; PID:CAA47799.1; PID:es1594; PID:g1333871

C/Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 86.7%; Score 13; DB 2; Length 9;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3

DB 6 GSY 8

RESULT 2

G41946

T-cell receptor gamma chain (2c.23) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C/Accession: G41946

R/Whetzel, M.; Mosley, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A/Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma g

A/Reference number: A41946; MUID:92049316; PMID:1658619

A/Accession: G41946

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-9 <WH>

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 86.7%; Score 13; DB 2; Length 9;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3

DB 3 GSY 5

RESULT 3

PT0250
 Ig heavy chain CRD3 region (clone 2-109B) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0250
 R/Yamada, M.; Messerman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rivera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A/Reference number: PT0222; PMID:91108337; PMID:1899102
 A/Accession: PT0250
 A/Molecule type: DNA
 A/Residues: 1-11 <YAM>
 A/Experimental source: B lymphocyte
 C/Keywords: heterotrimer; immunoglobulin

Query Match 86.7%; Score 13; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 8.1e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 Db 1 GTY 3

RESULT 4
 PT0214
 T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
 C/Accession: PT0214
 R/Nakano, N.; Kikuchi, H.; Nishimoto, H.; Kishimoto, T.
 J. Exp. Med. 173, 1091-1097, 1991
 A/Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted
 A/Reference number: PT0209; PMID:91217621; PMID:1902501
 A/Accession: PT0214
 A/Molecule type: mRNA
 A/Residues: 1-11 <NAX>
 C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 8.1e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 Db 5 GTY 7

RESULT 5
 A33099
 163K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
 C/Species: Plasmodium falciparum
 C/Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C/Accession: A33099
 R/Nichols, J.H.; Hager, L.P.
 Submitted to the Protein Sequence Database, May 1990
 A/Reference number: A33098
 A/Accession: A33099
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-12 <NTC>

Query Match 86.7%; Score 13; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 Db 9 GTY 11

RESULT 6
 S47391

T-cell antigen receptor VJ junction beta chain - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C/Accession: S47391; S47386
 R/Lehner, P.U.
 Submitted to the EMBL Data Library, August 1994
 A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T
 A/Reference number: S47355
 A/Accession: S47391
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-12 <LEH>
 A/Cross-references: EMBL:235712; NID:9527519; PIDD:CAA84784.1; PID:9527520; EMBL:235701
 C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 Db 6 GSY 8

RESULT 7
 S47395
 T-cell antigen receptor VJ junction beta chain - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C/Accession: S47395
 R/Lehner, P.U.
 Submitted to the EMBL Data Library, August 1994
 A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T
 A/Reference number: S47355
 A/Accession: S47395
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-12 <LEH>
 A/Cross-references: EMBL:235715; NID:9527525; PIDD:CAA84784.1; PID:9527526
 C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 Db 6 GSY 8

RESULT 8
 PH1611
 Ig H chain V-D-J region (wild-type clone 341) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1611
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A/Reference number: PH1580; PMID:93301609; PMID:8315387
 A/Accession: PH1611
 A/Molecule type: DNA
 A/Residues: 1-12 <LEV>
 A/Experimental source: bone marrow pre-B lymphocyte
 C/Keywords: immunoglobulin

Query Match 86.7%; Score 13; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 8.8e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 Db 5 GSY 7

RESULT 9

PH0802
T-cell receptor alpha chain (M2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0802
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0802
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X60910
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 6 GTY 8

RESULT 10

PH0790
T-cell receptor alpha chain (QB7.3.2 V-alpha-4.3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0790
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0790
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X60895
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 6 GTY 8

RESULT 11

S47368
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47368
R/Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A/Reference number: S47355
A/Accession: S47368
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:Z35693; NID:9527477; PIDN:CAA64762.1; PID:9527478
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 7 GAY 9

RESULT 12

S47383
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47383
R/Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A/Reference number: S47355
A/Accession: S47383
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:Z35709; NID:9527513; PIDN:CAA64778.1; PID:9527514
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 7 GSY 9

RESULT 13

PH0788
T-cell receptor alpha chain (E22 V-alpha-8.73.4) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0788
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0788
A/Molecule type: mRNA
A/Residues: 1-13 <CAS>
A/Cross-references: EMBL:X60893
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 7 GTY 9

RESULT 14

PQ0700
unidentified 6.3/40K protein (imported) - rice (fragment)
C/Species: Oryza sativa (rice)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: PQ0700
R/Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A/Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A/Reference number: PQ0696
A/Accession: PQ0700

A>Status: Preliminary
 A:Molecule type: Protein
 A:Residues: 1-13 <KOM>
 A:Cross-references: UNIPROT:Q7MLU1

Query Match 86.7%; Score 13; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 9.5e+02;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 |
 Db 3 GAY 5

RESULT 15

A59018 MUC1 enhancer binding protein 70k chain MUC1EBP-70 - human (fragment)

C:Species: Homo sapiens (man)
 C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998

C:Accession: A59018

R:Abn, M.; Smith, C.U.; Larson, C.J.

submitted to the Protein Sequence Database, May 1998

A:Description: Involvement of "Xu-like" proteins in the transcription of MUC1/DF3, a bre

A:Reference number: A59018

A:Accession: A59018

A:Molecule type: Protein

A:Residues: 1-14 <ABE>

A:Experimental source: breast cancer cell line MCF-7

A>Note: 3-Val was also found

C:Keywords: DNA binding; heterodimer

Query Match 86.7%; Score 13; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 |
 Db 6 GSY 8

Search completed: December 13, 2004, 22:32:59
 Job time : 15.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:00:41 / Search time 83.8 Seconds

(without alignments)
27.464 Million cell updates/sec

Title: US-10-068-905-7

Perfect score: 15

Sequence: 1 GXVX 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	86.7	8	1 UF06 MOUSE	P38644 mus musculu
2	13	86.7	9	2 Q9QWTO	Q9QWTO mus musculu
3	13	86.7	10	2 Q8NEV9	Q8NEV9 homo sapien
4	13	86.7	10	2 A8063472	A8063472 homo sapi
5	13	86.7	11	2 Q9UC46	Q9UC46 homo sapien
6	13	86.7	11	2 Q7YP62	Q7YP62 homo sapien
7	13	86.7	13	1 ADFB_TENNO	P83109 tenebrio mo
8	13	86.7	13	2 P82432	P82432 nicotiana t
9	13	86.7	13	2 Q7M1U1	Q7M1U1 cyzsa sativ
10	13	86.7	13	2 Q7Y0R1	Q7Y0R1 brassica ju
11	13	86.7	15	1 PH3_PRUSE	P39263 prunus sero
12	13	86.7	15	1 UC14_MAIZE	P80620 zea mays (m
13	13	86.7	15	2 Q9S814	Q9S814 zea mays (m
14	13	86.7	15	2 Q47892	Q47892 fremyella d
15	13	86.7	15	2 Q47893	Q47893 fremyella d
16	13	86.7	16	1 PH2_PRUSE	P39264 prunus sero
17	13	86.7	16	2 Q71GD2	Q71GD2 homo sapien
18	13	86.7	16	2 Q6UDK3	Q6UDK3 canis famli
19	13	86.7	16	2 Q9SMV3	Q9SMV3 arabidopsis
20	13	86.7	17	2 Q6LC19	Q6LC19 homo sapien
21	13	86.7	17	2 Q62645	Q62645 saguinus oe
22	13	86.7	17	2 Q71V04	Q71V04 homo sapien
23	13	86.7	17	2 Q9T2H6	Q9T2H6 spinnacia ol
24	13	86.7	17	2 Q84098	Q84098 influenza a
25	13	86.7	17	2 Q71ZNI	Q71ZNI torpedo mar
26	13	86.7	17	2 AAC39714	AAC39714 homo sapi
27	13	86.7	17	2 AAB92363	AAB92363 homo sapi
28	13	86.7	18	2 Q9GJM1	Q9GJM1 lagenorhync
29	13	86.7	18	2 Q9GJM2	Q9GJM2 lagenorhync
30	13	86.7	18	2 Q9GJM3	Q9GJM3 lagenorhync
31	13	86.7	18	2 Q6LD78	Q6LD78 clostridium

32	13	86.7	18	2 Q9R4C6	Q9R4C6 agrobacteri
33	13	86.7	18	2 Q9R4F9	Q9R4F9 aeromonas.
34	13	86.7	18	2 Q9R501	Q9R501 bacillus su
35	13	86.7	18	2 Q9PRX1	Q9PRX1 struchtio ca
36	13	86.7	18	2 AAB20893	AAB20893 clostridi
37	13	86.7	19	2 Q9N613	Q9N613 toxoplasma
38	13	86.7	19	2 Q9GNL6	Q9GNL6 drosophila
39	13	86.7	19	2 Q47895	Q47895 fremyella d
40	13	86.7	19	2 Q9R4F8	Q9R4F8 aeromonas.
41	13	86.7	19	2 Q9R6U8	Q9R6U8 yersinia pe
42	13	86.7	20	1 PYR_PYPAP	P37362 pyrrhocoris
43	13	86.7	20	2 Q25281	Q25281 leishmania
44	13	86.7	20	2 Q9GNL7	Q9GNL7 drosophila
45	13	86.7	20	2 Q9S8H8	Q9S8H8 brassica na

ALIGNMENTS

RESULT 1					
ID	UF06 MOUSE	STANDARD;	PRT;	8 AA.	
AC	P38644;				
DT	01-OCT-1994 (Rel. 30, Created)				
DT	01-OCT-1994 (Rel. 30, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Unknown protein from 2D-PAGE of fibroblasts (P50) (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RP	[1]				
RP	SEQUENCE:				
RC	TISUE=Fibroblast;				
RX	MEDLINE=95009907; PubMed=7523108;				
RA	Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;				
RT	"Separation and sequencing of familial and novel murine proteins using				
RL	Electrophoresis 15:735-745(1994)."				
CC	-I- MISCELLANEOUS: On the 2D-gel the determined pi of this unknown				
CC	protein is: 5.2, its MW is: 50 kDa.				
KW	Direct protein sequencing.				
FT	NON TER				
SO	SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;				
Query Match					
Best Local Similarity 86.7%; Score 13; DB 1; Length 8;					
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy	1 GXV 3				
Db	6 GAY 8				
RESULT 2					
ID	Q9QWTO;	PRELIMINARY;	PRT;	9 AA.	
AC	Q9QWTO;				
DT	01-MAY-2000 (TEMBREL. 13, Created)				
DT	01-MAY-2000 (TEMBREL. 13, Last sequence update)				
DT	01-DEC-2001 (TEMBREL. 19, Last annotation update)				
DE	Proteinase 3 (Myeloblastin) (Fragment).				
GN	Name=Prtn3;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=SV129 D3;				
RA	Lutz P.G., Moog-Lutz C., Houzel-Charavel A., Cayre Y.E.;				
RL	Submitted (JUN-1998) to the EMBL/Genbank/DBD databases.				
DR	EMBL; A007030; CAA07429.1; -.				

DR MGD; MGI:893580; Ptn3.
FT NON TER 9
SQ SEQUENCE 9 AA; 937 MW; C91E75A77B45B87D CRC64;

Query Match 86.7%; Score 13; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GSY 5

RESULT 3
ID Q9NEV9 PRELIMINARY; PRT; 10 AA.
AC Q9NEV9;

DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Type II hair-specific keratin (Type II hair keratin) (Fragment).
GN Name=KRTPB6;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RA Baitra N.K., Bamezai R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RA Baitra N.K., Bamezai R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY203963; AAK6688.1; -
DR GO; GO:0005882; C:intermediate filament; IEA.

KM Keratin.
FT NON TER 10
SQ SEQUENCE 10 AA; 1034 MW; 9B53417EAB45B87E CRC64;

Query Match 86.7%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GSY 6

RESULT 4
ID AAO63472 PRELIMINARY; PRT; 10 AA.
AC AAO63472;

DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Type II hair keratin (Fragment).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RA Baitra N.K., Bamezai R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY203963; AAO63472.1; -
KM Keratin.
FT NON TER 10
SQ SEQUENCE 10 AA; 1034 MW; 9B53417EAB45B87E CRC64;

Query Match 86.7%; Score 13; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GSY 6

RESULT 5
ID Q9UC46 PRELIMINARY; PRT; 11 AA.
AC Q9UC46;

DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Neutrophil inhibitor peptide, NIP-POLYMOBPHONUCLEAR neutrophil inhibitor peptide.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE.
RX MEDLINE=96326114; PubMed=8703476;
RA Cooper J.A., Culbreth R.R.;
RL "Characterization of a neutrophil inhibitor peptide harvested from human bronchial lavage: homology to influenza A nucleoprotein."

RT Am. J. Respir. Cell Mol. Biol. 15:207-215(1996).
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0030236; P:anti-inflammatory response; NAS.

SQ SEQUENCE 11 AA; 1262 MW; 951A1C3279C5DB45 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 7.2e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GSY 5

RESULT 6
ID Q7YP62 PRELIMINARY; PRT; 11 AA.
AC Q7YP62;

DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MHC class Ib antigen (Fragment).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., He X., Xu L., Zeng Y.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY328516; AAP94210.1; -
FT NON TER 1
SQ SEQUENCE 11 AA; 1208 MW; 2B0B6C5CC5AB45B8 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 7.2e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GSY 6

RESULT 7
ADFB_TEMMO

ID ADFR-TEMPO STANDARD; PRT: 13 AA.
 AC P83109;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Antidiuretic factor B (ADFb).
 OS Tenebrio molitor (Yellow mealworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tenebrio.
 NCBI_TaxID=7067;
 RN [1]
 RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=22465067; PubMed=12576082;
 RA Eigenheer R.A., Wierhart U.M., Nicolson S.W., Schoofs L., Schegg K.M., Hall J.J., Schooley D.A.;
 RT "Isolation, identification and localization of a second beetle antidiuretic peptide."
 RL Peptides 24:27-34(2003).
 CC -1- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses CGMP as second messenger. May function as an antidiuretic hormone.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two pairs of bilaterally symmetrical cells in the protocerebrum.
 CC -1- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI; RANGE=1-13;
 CC NOTE=Ref.1.
 KW Direct protein sequencing; Hormone; Neuropeptide.
 SQ SEQUENCE 13 AA; 1562 MW; 0240450458A632B CRC64;
 QY Query Match 86.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 GXY 3
 4 GSY 6
 RESULT 8
 ID P82432 PRELIMINARY; PRT: 13 AA.
 AC P82432;
 DT 01-JUN-2000 (TRENBLrel. 14, Created)
 DT 01-JUN-2000 (TRENBLrel. 14, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE 32 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; OC Lamiales; Solanales; Solanaceae; Nicotiana.
 NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R., Wojtaszek P., Botwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed tobacco culture."
 RL Planta 0:0-0(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL.
 CC -1- TISSUE SPECIFICITY: XYLEM.
 DR GO: GO:0005618; C:cell wall; IEA.
 KW Cell wall.
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1307 MW; D5022297D8697DC6 CRC64;
 QY Query Match 86.7%; Score 13; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 GXY 3

Db 9 GAY 11
 RESULT 9
 ID Q7Y0R1 PRELIMINARY; PRT: 13 AA.
 AC Q7Y0R1;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Unidentified 6.3/40K protein (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RA Komatsu S., Kajiwara H., Hirano H.;
 RT "A rice protein library, a data file of rice proteins separated by two-dimensional electrophoresis."
 RL Theor. Appl. Genet. 86:935-942(1993).
 DR PIR; P00700; P00700.
 FT NON TER 1
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1218 MW; 27BA7291E7D3DB878 CRC64;
 QY Query Match 86.7%; Score 13; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 GXY 3
 3 GAY 5
 RESULT 10
 ID Q7Y0R1 PRELIMINARY; PRT: 13 AA.
 AC Q7Y0R1;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Gamma-glutamylcysteine synthetase (EC 6.3.2.2) (Fragment).
 GN Name=gsn1;
 OS Brassica juncea (leaf mustard) (Indian mustard).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC Eurosid II; Brassicales; Brassicaceae; Brassica.
 NCBI_TaxID=3707;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wächter A., Steininger H., Rausch T., Bögs J.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AA564376; CND91995.1;
 DR GO: GO:0004357; F:glutamate-cysteine ligase activity; IEA.
 DR GO: GO:0016874; F:ligase activity; IEA.
 KW Ligase.
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1266 MW; DBF2097182417DC6 CRC64;
 QY Query Match 86.7%; Score 13; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 GXY 3
 9 GAY 11
 RESULT 11
 PH3_PRUSE

ID PH3_PRUBS STANDARD; PRT; 15 AA.
 AC P29265;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Prunasin beta-glucosidase IIB (EC 3.2.1.118) (Prunasin hydrolase isoform IIB) (Fragment).
 OS Prunus serotina (Black cherry).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid1; Rosales; Rosaceae; Amygdaloideae; Prunus.
 NCBI_TaxID=23207;
 RX [1]
 RN NCBI
 RP SEQUENCE
 RC TISSUE=Seed.
 RA Li C.P., Swain E., Poulton J.E.;
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase";
 RL Plant Physiol. 100:282-290 (1992).
 CC -1- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-glucose.
 CC -1- SUBUNIT: Monomer.
 CC -1- DEVELOPMENTAL STAGE: Absent from maturing black cherry fruits until 6 weeks after flowering. Then, concomitant with cotyledon development, the level of enzyme increases with specificity for embryonal tissues.
 CC -1- PFM: Glycosylated.
 CC Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
 KW Multigene family.
 FT NON_TER
 FT SEQUENCE 15 AA; 1635 MW; 493D7F4FB90CFB4C CRC64;

Query Match 86.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 DB 1 GXY 3

RESULT 12
 UC14_MAIZE STANDARD; PRT; 15 AA.
 ID UC14_MAIZE
 AC P80620;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 258) (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 NCBI_TaxID=4577;
 RX [1]
 RN NCBI
 RP SEQUENCE
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Dameval C., Huet J.-C., Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005 (1996).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 5.9, its MW is: 34.6 kDa.
 DR Maize-2DPAGE; P80620; COLEOPTILE.
 DR MaizeDB; 123944; -;
 KW Direct protein sequencing.
 FT NON_TER
 FT SEQUENCE 15 AA; 1564 MW; CFOBBA0B7DE658 CRC64;
 SQ SEQUENCE 15 AA; 1564 MW; CFOBBA0B7DE658 CRC64;

Query Match 86.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 GXY 3
 DB 7 GXY 9

RESULT 13
 ID Q958L4 PRELIMINARY; PRT; 15 AA.
 AC Q958L4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Beta-D-glucoside glucosyltransferase (EC 3.2.1.21) (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 NCBI_TaxID=4577;
 RX [1]
 RN NCBI
 RP SEQUENCE
 RC MEDLINE=94347094; PubMed=8068000;
 RA Feldman J., Venter A., Zetl R., Bako L., Campos N., Palme K.;
 RT "Characterization of two membrane-associated beta-glucosidases from maize (Zea mays L.) coleoptiles";
 RL Biochem. J. 302:15-21 (1994).
 DR GO:0008422; F:beta-glucosidase activity; IEA.
 SQ SEQUENCE 15 AA; 1667 MW; 46C40370DC8C730B CRC64;

Query Match 86.7%; Score 13; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 DB 3 GXY 5

RESULT 14
 ID Q47892 PRELIMINARY; PRT; 15 AA.
 AC Q47892;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Beta-allophycocyanin (Fragment).
 OS Fremyella diplosiphon (Calothrix PCC 7601).
 OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
 NCBI_TaxID=1197;
 RX [1]
 RN NCBI
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86233345; PubMed=3086870;
 RA Conley P.B., Lemaux P.G., Lomax T.L., Grossman A.R.;
 RT "Genes encoding major light-harvesting polypeptides are clustered on the genome of the cyanobacterium Fremyella diplosiphon";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928 (1986).
 DR EMBL: M13216; AAA24871.1; -;
 FT NON_TER
 FT SEQUENCE 15 AA; 1644 MW; 9727165659F462F CRC64;

Query Match 86.7%; Score 13; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GXY 3
 DB 4 GXY 6

RESULT 15
 ID Q47893 PRELIMINARY; PRT; 15 AA.

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us-10-068-905-7.rup

Page 5

AC 047893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
DE Beta-phycocyanin (Fragment).
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
OX NCBI_TaxID=1197;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86233345; PubMed=3086870;
RA Conley P.B., Lemaux P.G., Lomax T.L., Groseman A.R.;
RT "Genes encoding major light-harvesting polypeptides are clustered on
the genome of the cyanobacterium Fremyella diplosiphon.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928(1986).
DR EMBL; M13217; AAA24880.1; -;
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1528 MM; 7FF2F65518F493D4 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 9.4e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GST 6

Search completed: December 13, 2004, 22:31:37
Job time : 84.8 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 21:59:41 ; Search time 80 Seconds
(without alignments)
17,936 Million cell updates/sec

Title: US-10-068-905-8

Perfect score: 15
Sequence: 1 GXYX 4

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseq_23Sep04:*
2: Genesep1980s:*
3: Genesep2000s:*
4: Genesep2001s:*
5: Genesep2002s:*
6: Genesep2003as:*
7: Genesep2003bs:*
8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	86.7	4	1 AAP61656	AAP61656 Sequence
2	13	86.7	4	1 AAP71313	AAP71313 Peptide c
3	13	86.7	4	1 AAR55333	AAR55333 Inhibitor
4	13	86.7	4	2 AAR55499	AAR55499 Csa recep
5	13	86.7	4	5 ABP55713	ABP55713 B15 class
6	13	86.7	4	5 ABP55796	ABP55796 B15 class
7	13	86.7	4	5 ABG96845	ABG96845 Human leu
8	13	86.7	4	5 ABG97024	ABG97024 Human leu
9	13	86.7	4	5 ABG96697	ABG96697 Human CD6
10	13	86.7	4	5 ABP67653	ABP67653 Human CD6
11	13	86.7	4	5 AAB84247	AAB84247 Caspase c
12	13	86.7	4	6 ABP59243	ABP59243 ErbB rece
13	13	86.7	4	7 ADJ181984	ADJ181984 Peptide e
14	13	86.7	4	7 ADL98858	ADL98858 Thermus b
15	13	86.7	4	7 ADL98369	ADL98369 Human leu
16	13	86.7	4	7 ADL98514	ADL98514 Human leu
17	13	86.7	4	7 ADL98514	ADL98514 Human leu
18	13	86.7	4	7 ADL98514	ADL98514 Human leu
19	13	86.7	4	7 ADL98514	ADL98514 Human leu
20	13	86.7	4	8 ADK42068	ADK42068 Antihpase
21	13	86.7	4	8 AAR34342	AAR34342 Ro/SSA ep
22	13	86.7	5	2 AAR56301	AAR56301 Second ge
23	13	86.7	5	2 AAR56298	AAR56298 Synthetic
24	13	86.7	5	2 AAR72555	AAR72555 Pertussis
25	13	86.7	5	2 AAR72555	AAR72555 Pertussis

26	13	86.7	5	2 AAR72549	AAR72549 Pertussis
27	13	86.7	5	2 AAR72699	AAR72699 kappa-cas
28	13	86.7	5	2 AAY1820	AAY1820 Pertussis
29	13	86.7	5	2 AAY1826	AAY1826 Pertussis
30	13	86.7	5	2 AAY95230	AAY95230 PT toxin
31	13	86.7	5	2 AAY95236	AAY95236 PT toxin
32	13	86.7	5	2 AAY43373	AAY43373 Pertussis
33	13	86.7	5	2 AAY43367	AAY43367 Pertussis
34	13	86.7	5	3 AAY44679	AAY44679 Pertussis
35	13	86.7	5	3 AAY68369	AAY68369 Pertussis
36	13	86.7	5	3 AAY68375	AAY68375 Pertussis
37	13	86.7	5	3 AAB08397	AAB08397 Peptide d
38	13	86.7	5	4 AAB66243	AAB66243 B pertuss
39	13	86.7	5	4 AAB66249	AAB66249 B pertuss
40	13	86.7	5	5 ABP67641	ABP67641 Human CD6
41	13	86.7	5	5 ABP67642	ABP67642 Human CD6
42	13	86.7	5	5 AAE16333	AAE16333 N-termina
43	13	86.7	5	5 ABE75621	ABE75621 Anti-RANK
44	13	86.7	5	6 ABJ18639	ABJ18639 ErbB rece
45	13	86.7	5	6 ABP59244	ABP59244 Peptide e

ALIGNMENTS

RESULT 1	
AAP61656	AAP61656 standard; protein; 4 AA.
ID	XX
XX	XX
AC	AAP61656;
XX	XX
DT	25-MAR-2003 (revised)
DT	03-OCT-2002 (revised)
DT	21-AUG-1991 (first entry)
XX	XX
DE	Sequence of peptide which inhibits cyclic-nucleotide independent protein
DE	kinase activity and mammalian cell growth.
XX	XX
KW	Cell growth inhibitor; tumour cell growth inhibitor.
OS	Synthetic.
XX	XX
FT	Key
FT	Misc-difference 1 Location/Qualifiers
FT	Misc-difference 4 /label= Carboxyoxo-Phe
FT	Misc-difference 4 /label= Tyr-CH2Cl
XX	XX
PN	US4582821-A.
XX	XX
PD	15-APR-1986.
XX	XX
PR	16-NOV-1983; 83US-00552255.
XX	XX
PR	16-NOV-1983; 83US-00552255.
XX	XX
PA	(DUPO) DU POINT DE MEMOURS & CO E I.
XX	XX
PI	Ketner CA, Racker E;
XX	XX
DR	WPI, 1986-118872/18.
XX	XX
PT	Inhibition of tumour cell growth - using peptide and aminoacid
PT	halo:methyl ketone(s).
XX	XX
PS	Claim 1; Col 4; 9pp; English.
CC	The cpds. of the invention inhibit protein phosphorylation. The inventors
CC	claim a process for inhibiting the growth of tumour cells in a medium
CC	which comprises contacting the cells with a cpd. of formula (AAP61654-
CC	P61661) or a physiologically acceptable salt. (Updated on 03-OCT-2002 to
CC	add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX	XX

SQ Sequence 4 AA;
 Query Match 86.7%; Score 13; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 DB 2 GAY 4
 RESULT 2
 ID AAR71313 standard; protein; 4 AA.
 AC AAR71313;
 DT 25-MAR-2003 (revised)
 DT 15-MAY-1991 (first entry)
 DE Peptide component of cpd. for treating picornavirus infections.
 XX Picornaviridae; poliovirus; rhinovirus; antiviral agent.
 XX Synthetic.
 OS US4636492-A.
 PN 13-JAN-1987.
 PD 29-AUG-1984; 84US-00645426.
 PF 29-AUG-1984; 84US-00645426.
 PR 29-AUG-1984; 84US-00645426.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX PI Kettner CA, Korant BD;
 XX DR WPI; 1987-036897/05.
 PT Treating picorna-virus infection with peptide halo:methyl ketone cpds.
 PT esp. for treating polio virus and rhino virus infections.
 XX Disclosure; Page 4; 10pp; English.
 XX CC This peptide is useful as part of a peptide/halo-methyl ketone cpd., for
 CC treating picornavirus, esp. polio- or rhinovirus infections. It inhibits the
 CC processing of picornavirus capsid proteins by virus encoded proteases.
 CC See AAR71301-12. See also US4652552. (Updated on 25-MAR-2003 to correct
 CC PA field.)
 CC XX
 SQ Sequence 4 AA;
 Query Match 86.7%; Score 13; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 DB 2 GAY 4
 RESULT 3
 ID AAR55333 standard; peptide; 4 AA.
 AC AAR55333;
 DT 25-MAR-2003 (revised)
 DT 30-JAN-1995 (first entry)
 DE Inhibitor of tyrosine kinase.
 XX

KW PTK; signal transduction; proliferation; cancer; psoriasis; viral;
 KW inflammatory; allergic; cardiovascular; diseases.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 3 /note="Tyr(2,3,5,6-P4) (D/L)"
 FT FT
 XX
 PN MO9411392-A1.
 PD 26-MAY-1994.
 PF 03-NOV-1993; 93WO-US010610.
 PR 06-NOV-1992; 92US-00973136.
 PR 27-OCT-1993; 93US-00139913.
 XX (WARN) WARNER LAMBERT CO.
 XX PA Dobrusin EM, Mcnamara DJ, Fry DW, Singh J;
 XX PI WPI; 1994-183419/22.
 XX DR
 XX PT New peptide inhibitors of protein tyrosine kinase - contain D-Tyr or
 PT tetrafluoro-Tyr residue, for treating proliferative diseases, viral
 PT infection, inflammation etc.
 XX PS Claim 7; Page 36; 44pp; English.
 XX CC The sequence is that of a protein tyrosine kinase inhibitor contg. D- Tyr
 CC or tetrafluoro-Tyr residues. The peptide can be used to inhibit TK-
 CC mediated signal transduction and is useful for controlling proliferative
 CC diseases, e.g. cancer, psoriasis and to treat viral, inflammatory,
 CC allergic and cardiovascular diseases. See also AAR5302-39. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 CC XX
 SQ Sequence 4 AA;
 Query Match 86.7%; Score 13; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 DB 1 GAY 3
 RESULT 4
 ID AAR75499 standard; peptide; 4 AA.
 AC AAR75499;
 DT 25-MAR-2003 (revised)
 DT 13-NOV-1995 (first entry)
 DE C5a receptor-antagonist core tetrapeptide.
 XX C5a; C5a receptor-antagonist; antiinflammatory.
 XX Homo sapiens.
 OS WO9516033-A1.
 PN 15-JUN-1995.
 PD 16-NOV-1994; 94WO-IB000359.
 PR 06-DEC-1993; 93US-00162591.
 XX (CIBA) CIBA GEIGY AG.
 XX

PI Van Oostrom J, Boyar WC, Galakatos NG, Peppard JV;
 XX WPI; 1995-224319/29.
 DR
 XX C5a receptor antagonists having no agonist activity - are used in
 XX compns. to treat C5a-mediated diseases and inflammatory conditions.
 PT
 XX Disclosure; Page 36; 65pp; English.
 PS
 XX Polypeptide receptor antagonists to C5a contain an essential core
 CC tetrapeptide (AAR75498 or AAR75499) or core tripeptide (DGA) which
 CC displays C5a blocking activity. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 CC
 XX Sequence 4 AA;
 SQ

Query Match 86.7%; Score 13; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 | |
 2 GAY 4

RESULT 5
 ABP55713
 ID ABP55713 standard; peptide; 4 AA.
 XX
 AC ABP55713;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE B15 class I sHLA molecule ligand related peptide #7.
 XX
 KW HLA ligand; human leukocyte antigen; predictive algorithm; database;
 KM MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
 XX
 OS Synthetic.
 XX
 PN WO200269198-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 21-FEB-2002; 2002WO-US005298.
 XX
 PR 21-FEB-2001; 2001US-0270357P.
 PR 10-OCT-2001; 2001US-00974366.
 PR 18-DEC-2001; 2001US-00022066.
 XX
 PA (HILD/) HILDEBRAND W H.
 PA (PRIL/) PRILLIMAN K R.
 PA (HICK/) HICKMAN H D.
 XX
 PI Hildebrand WH, Prilliman KR, Hickman HD;
 XX WPI; 2002-732755/79.
 DR
 XX Human leukocyte antigen ligand database assembled by producing HLA having
 PT loaded ligands, isolating and sequencing loaded ligands to obtain HLA
 PT ligand data and populating database in computer system with ligand data.
 XX
 PS Disclosure; Fig 5; 118pp; English.

CC The present invention describes a human leukocyte antigen (HLA) (e.g.
 CC soluble HLA) ligand database assembled by a process which involves
 CC providing a computer system capable of storing HLA data as a database,
 CC producing HLA having ligands loaded on it, isolating the loaded ligands
 CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
 CC populating the database with HLA ligand data. Also described: (1)
 CC accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
 CC system for HLA (e.g. sHLA) ligand database. The database is populated
 CC with HLA ligand sequences, motifs, extended motifs, submotifs, ligands

CC unique to infected cells, tumour specific ligands, as well as a
 CC collection of current and future developed HLA ligand sequences. The
 CC database which contains endogenously bound and loaded ligands facilitates
 CC searching of viral, bacterial, tumour or human protein sequences for
 CC ligands likely to bind a particular HLA class I or class II protein. The
 CC database allows the user to screen an unknown peptide sequence for
 CC potential matches with sHLA ligand discrete sequences or sHLA ligand
 CC motifs of sequences. Due to the completeness and concentration of sHLA
 CC obtained to date, better sequencing data of numerous endogenously loaded
 CC HLA ligands is found in the sHLA ligand database, and by comparison of
 CC such ligands to each other and to the genomic sequence, better motifs are
 CC also found in the sHLA ligand database. ABP55692 to ABP55912 represent
 CC amino acid sequences used in the exemplification of the present invention
 CC
 XX Sequence 4 AA;
 SQ

Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 | |
 2 GAY 4

RESULT 6
 ABP55796
 ID ABP55796 standard; peptide; 4 AA.
 XX
 AC ABP55796;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE B15 class I sHLA molecule ligand related peptide #90.
 XX
 KW HLA ligand; human leukocyte antigen; predictive algorithm; database;
 KM MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
 XX
 OS Synthetic.
 XX
 PN WO200269198-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 21-FEB-2002; 2002WO-US005298.
 XX
 PR 21-FEB-2001; 2001US-0270357P.
 PR 10-OCT-2001; 2001US-00974366.
 PR 18-DEC-2001; 2001US-00022066.
 XX
 PA (HILD/) HILDEBRAND W H.
 PA (PRIL/) PRILLIMAN K R.
 PA (HICK/) HICKMAN H D.
 XX
 PI Hildebrand WH, Prilliman KR, Hickman HD;
 XX WPI; 2002-732755/79.
 DR
 XX Human leukocyte antigen ligand database assembled by producing HLA having
 PT loaded ligands, isolating and sequencing loaded ligands to obtain HLA
 PT ligand data and populating database in computer system with ligand data.
 XX
 PS Disclosure; Fig 5; 118pp; English.

CC The present invention describes a human leukocyte antigen (HLA) (e.g.
 CC soluble HLA) ligand database assembled by a process which involves
 CC providing a computer system capable of storing HLA data as a database,
 CC producing HLA having ligands loaded on it, isolating the loaded ligands
 CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
 CC populating the database with HLA ligand data. Also described: (1)
 CC accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
 CC system for HLA (e.g. sHLA) ligand database. The database is populated
 CC with HLA ligand sequences, motifs, extended motifs, submotifs, ligands

CC unique to infected cells, tumour specific ligands, as well as a
CC collection of current and future developed HLA ligand sequences. The
CC database which contains endogenously bound and loaded ligands facilitates
CC searching of viral, bacterial, tumour or human protein sequences for
CC ligands likely to bind a particular HLA class I or class II protein. The
CC database allows the user to screen an unknown peptide sequence for
CC potential matches with SHLA ligand discrete sequences or SHLA ligand
CC motifs of sequences. Due to the completeness and concentration of SHLA
CC obtained to date, better sequencing data of numerous endogenously loaded
CC HLA ligands is found in the SHLA ligand database, and by comparison of
CC such ligands to each other and to the genomic sequence, better motifs are
CC also found in the SHLA ligand database. ABP55692 to ABP55912 represent
CC amino acid sequences used in the exemplification of the present invention
XX
SQ Sequence 4 AA;
Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GXY 3
DB 2 GAY 4
RESULT 7
ABG96845
ID ABG96845 standard; peptide; 4 AA.
XX
AC ABG96845;
XX
DT 16-DEC-2002 (first entry)
XX
DE Human leukocyte antigen (HLA) B15 ligand #170.
XX
KM Soluble human leukocyte antigen; HLA; SHLA; cell pharm;
XX multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
XX viral infection; cancer; autoimmune disease; vaccine development; MHC;
XX major histocompatibility complex; diagnostic development;
XX HLA class I polymorphism; HLA-B15 allele; ligand.
XX
OS Homo sapiens.
XX
PN WO200262846-A2.
XX
PD 15-AUG-2002.
XX
PF 18-DEC-2001; 2001WO-US049744.
XX
PR 18-DEC-2000; 2000US-0256409P.
XX 18-DEC-2000; 2000US-0256410P.
XX 10-OCT-2001; 2001US-00974366.
XX
PA (HILD/) HILDEBRAND W H.
XX (PRIL/) PRILLIMAN K R.
XX
PI Hildebrand WH, Prilliman KR;
XX
DR WPI; 2002-698563/75.
XX
PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
XX studies of peptide loading for characterizing human immune responses
XX involves using HLA allelic cDNA or genomic DNA as starting material.
XX
PS Disclosure; Page 178; 300pp; English.
XX
CC The invention describes a method of producing soluble human leukocyte
CC antigen (HLA) molecules (SHLA) in cell pharm involving amplifying HLA
CC allelic DNA by PCR using a locus specific primer to produce truncated a
CC PCR product (PI), inserting PI into mammalian expression vector;
CC electroporating the plasmid into a host cell; inoculating the cell pharm
CC with the host cell such that cell pharm produces SHLA. A multimeric HLA
CC complex (I) is useful for testing functionality of peptide ligands bound

CC by at least two soluble HLA molecules. (I) can be tested for its ability
CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
CC responses in humans. (I) is useful for studying T cell responses to
CC pathological conditions such as viral infections and cancer, and for
CC modulating the human immune system to induce tolerance in autoimmune
CC diseases. The individual secreted major histocompatibility complex (MHC)
CC molecules produced are useful for studies of peptide loading (i.e., in
CC vaccine development) and to the development of diagnostics. With the
CC secreted MHC molecules, naturally loaded peptides can be eluted from the
CC MHC molecule and characterized. The secreted MHC molecules allow the
CC assessment of structural and functional impact of HLA class I
CC polymorphism. The molecules are also useful to generate ligands and hence
CC ligand maps from the peptide pools extracted from series of distinct yet
CC related class I HLA-B15 alleles; compare the different ligand maps to
CC identify potentially shared elements; and characterize the elements
CC identified to positively or negatively validate the occurrence of
CC overlapping ligands. The truncated version of (MHC) can be produced in
CC mammalian or insect/bacterial cells such that milligram or greater
CC quantities of an individual class I or class II molecule can be obtained.
CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
XX
SQ Sequence 4 AA;
Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GXY 3
DB 2 GAY 4
RESULT 8
ABG97024
ID ABG97024 standard; peptide; 4 AA.
XX
AC ABG97024;
XX
DT 16-DEC-2002 (first entry)
XX
DE Human leukocyte antigen (HLA) B15 ligand #352.
XX
KM Soluble human leukocyte antigen; HLA; SHLA; cell pharm;
XX multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
XX viral infection; cancer; autoimmune disease; vaccine development; MHC;
XX major histocompatibility complex; diagnostic development;
XX HLA class I polymorphism; HLA-B15 allele; ligand.
XX
OS Homo sapiens.
XX
PN WO200262846-A2.
XX
PD 15-AUG-2002.
XX
PF 18-DEC-2001; 2001WO-US049744.
XX
PR 18-DEC-2000; 2000US-0256409P.
XX 18-DEC-2000; 2000US-0256410P.
XX 10-OCT-2001; 2001US-00974366.
XX
PA (HILD/) HILDEBRAND W H.
XX (PRIL/) PRILLIMAN K R.
XX
PI Hildebrand WH, Prilliman KR;
XX
DR WPI; 2002-698563/75.
XX
PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
XX studies of peptide loading for characterizing human immune responses
XX involves using HLA allelic cDNA or genomic DNA as starting material.
XX
PS Disclosure; Page 183; 300pp; English.
XX

The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules (SHLA) in cell pharm involving amplifying HLA allelic DNA by PCR using a locus specific primer to produce truncated a PCR product (P1), inserting P1 into mammalian expression vector; electroporating the plasmid into a host cell; inoculating the cell pharm with the host cell such that cell pharm produces SHLA. A multimeric HLA complex (I) is useful for testing functionality of peptide ligands bound by at least two soluble HLA molecules. (I) can be tested for its ability to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune responses in humans. (I) is useful for studying T cell responses to pathological conditions such as viral infections and cancer, and for modulating the human immune system to induce tolerance in autoimmune diseases. The individual secreted major histocompatibility complex (MHC) molecules produced are useful for studies of peptide loading (i.e., in vaccine development) and to the development of diagnostics. With the secreted MHC molecules, naturally loaded peptides can be eluted from the MHC molecule and characterized. The secreted MHC molecules allow the assessment of structural and functional impact of HLA class I polymorphism. The molecules are also useful to generate ligands and hence ligand maps from the peptide pools extracted from series of distinct yet related class I HLA-B*5 alleles; compare the different ligand maps to identify potentially shared elements; and characterize the elements identified to positively or negatively validate the occurrence of overlapping ligands. The truncated version of (MHC) can be produced in mammalian or insect/bacterial cells such that milligram or greater quantities of an individual class I or class II molecule can be obtained. This sequence represents a HLA (human leukocyte antigen) peptide ligand

```

Query Match      86.7%   Score 13;   DB 5;   Length 4;
Best Local Similarity 66.7%;   Pred. No. 1.7e+06;
Matches      2;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

QY      1 GXY 3
        | |
        | |
Nb      2 GAY 4

```

RESULT	
ID	ABG96697
ID	ABG96697 standard; peptide, 4 AA.
AC	ABG96697;
DT	16-DEC-2002 (first entry)
DE	Human leukocyte antigen (HLA) B15 ligand #120.
XX	Soluble human leukocyte antigen; HLA; sHLA; cell pharm; multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response; viral infection; cancer; autoimmune disease; vaccine development; MHC; major histocompatibility complex; diagnostic development; HLA class I polymorphism; HLA-B15 allotype; ligand.
XX	Homo sapiens.
XX	MO200262846-AA2.
PN	15-AUG-2002.
PD	18-DEC-2001; 2001WO-US049744.
PF	18-DEC-2000; 2000US-0256409P.
XX	18-DEC-2000; 2000US-0256410P.
PPR	10-OCT-2001; 2001US-00974366.
XX	(HILD/) HILDBRAND W H. (PRIL/) PRILLIMAN K R.
PA	Hildebrand WH, Prilliman KR;
PFI	WPI; 2002-698563/75.
XX	

XX Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
PT studies of peptide loading for characterizing human immune responses
PT involves using HLA allelic cDNA or genomic DNA as starting material.
XX
ES Disclosure, Fig 26; 300pp; English.

The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules (sHLA) in cell pharms involving amplifying HLA allelic DNA by PCR using a locus specific primer to produce truncated a PCR product (Pt), inserting Pt into mammalian expression vector; electroporating the plasmid into a host cell; inoculating the cell pharm with the host cell such that cell pharm produces sHLA. A multimeric HLA complex (I) is useful for testing functionality of peptide ligands bound by at least two soluble HLA molecules. (I) can be tested for its ability to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune responses in humans. (I) is useful for studying T cell responses to pathological conditions such as viral infections and cancer, and for modulating the human immune system to induce tolerance in autoimmune diseases. The individual secreted major histocompatibility complex (MHC) molecules produced are useful for studies of peptide loading (I.e., in vaccine development) and to the development of diagnostics. With the secreted MHC molecules, naturally loaded peptides can be eluted from the MHC molecule and characterised. The secreted MHC molecules allow the assessment of structural and functional impact of HLA class I polymorphism. The molecules are also useful to generate ligands and hence ligand maps from the peptide pools extracted from series of distinct yet related class I HLA-B*5 alleles; compare the different ligand maps to identify potentially shared elements; and characterise the elements identified to positively or negatively validate the occurrence of overlapping ligands. The truncated version of (MHC) can be produced in mammalian or insect/bacterial cells such that milligram or greater quantities of an individual class I or class II molecule can be obtained. This sequence represents a HLA (human leukocyte antigen) peptide ligand

Query Match	86.7%	Score 13	DB 5	Length 4
Best Local Similarity	66.7%	Pred. No. 1.7e+06		
Matches	2	Conservative	0	Mismatches 1
				Indels 0
QY	1 GAY 3			
DB	2 GAY 4			
RESULT 10				
ID	ABP67652			
ID	ABP67652 standard; peptide: 4 AA.			
AC	ABP67652;			
XX				
DE	10-DEC-2002 (first entry)			
XX				
XX				
Human CD66 family modulating peptide SEQ ID NO 523.				
Human; CD66; CECAM; cytostatic; antiinflammatory; immunomodulator;				
antibacterial; virucide; gene therapy; vaccine; neutrophil;				
immune system; autoimmune disease; cancer; infection; bacterial; virus;				
inflammatory disease; transplantation; immunisation.				
XX				
Homo sapiens.				
OS				
XX				
PN	WO200268601-A2.			
XX				
PD	06-SEP-2002.			
XX				
EF	27-FEB-2002; 2002WC-US005720.			
XX				
FR	28-FEB-2001; 2001US-0272113P.			
XX				
(SKUB//) SKUBITZ K M.				
PA	(SKUB//) SKUBITZ A P N.			
XX				

XX Skubitz KM, Skubitz APN;
 PT WPI; 2002-706981/76.
 XX
 XX New peptide from a surface exposed region of a CD66 family member, useful
 PT for modulating the function of CD66 family members, e.g. activation of
 PT neutrophils, for treating or diagnosing autoimmune diseases or cancer,
 PT and as a vaccine.
 XX
 XX Claim 2; Page 30; 96pp; English.
 XX
 XX The invention relates to an isolated peptide (I) from a surface exposed
 CC region of a CD66 family member (ABP67130-ABP67990). The peptide
 CC modulates: (a) activation of neutrophils; (b) activation or inhibition of
 CC T-cells, B-cells, NK cells, LAK cells, dendritic cells or other immune
 CC system cells; (c) proliferation and/or differentiation of the above
 CC cells, including epithelial cells; (d) homotypic and/or heterotypic
 CC adhesion among CD66 family members; and (e) adhesion of CD66 family
 CC members to other ligands. The peptide is useful in modulating the
 CC function of CD66 family members and/or their ligands, such as activation
 CC of neutrophils and activation, inhibition, proliferation and/or
 CC differentiation of the immune cells. The peptides may also be used in
 CC treating or diagnosing autoimmune diseases, cancer, infections (e.g.
 CC bacterial or viral) or inflammatory diseases, in transplantation
 CC therapies and for immunisation
 CC
 SQ Sequence 4 AA;
 Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 1
 2 GSY 4
 Db
 RESULT 11
 ABP67653
 ID ABP67653 standard; peptide; 4 AA.
 XX
 AC ABP67653;
 XX
 XX 10-DEC-2002 (first entry)
 DT
 XX
 DE Human CD66 family modulating peptide SEQ ID NO 524.
 XX
 KW Human; CD66; CEACAM; cytosolic; anti-inflammatory; immunomodulator;
 KW antibacterial; virucide; gene therapy; vaccine; neutrophil;
 KW immune system; autoimmune disease; cancer; infection; bacterial; virus;
 KW inflammatory disease; transplantation; immunisation.
 XX
 OS Homo sapiens.
 XX
 PN WO200268601-A2.
 PD
 XX 06-SEP-2002.
 PD
 XX 27-FEB-2002; 2002WO-US005720.
 PF
 XX 28-FEB-2001; 2001US-0272113P.
 PR
 XX (SKUB/) SKUBITZ K M.
 PA (SKUB/) SKUBITZ A P N.
 XX
 XX Skubitz KM, Skubitz APN;
 PI
 XX WPI; 2002-706981/76.
 XX
 XX New peptide from a surface exposed region of a CD66 family member, useful
 PT for modulating the function of CD66 family members, e.g. activation of
 PT neutrophils, for treating or diagnosing autoimmune diseases or cancer,
 PT

PT and as a vaccine.
 XX
 XX Claim 2; Page 30; 96pp; English.
 XX
 XX The invention relates to an isolated peptide (I) from a surface exposed
 CC region of a CD66 family member (ABP67130-ABP67990). The peptide
 CC modulates: (a) activation of neutrophils; (b) activation or inhibition of
 CC T-cells, B-cells, NK cells, LAK cells, dendritic cells or other immune
 CC system cells; (c) proliferation and/or differentiation of the above
 CC cells, including epithelial cells; (d) homotypic and/or heterotypic
 CC adhesion among CD66 family members; and (e) adhesion of CD66 family
 CC members to other ligands. The peptide is useful in modulating the
 CC function of CD66 family members and/or their ligands, such as activation
 CC of neutrophils and activation, inhibition, proliferation and/or
 CC differentiation of the immune cells. The peptides may also be used in
 CC treating or diagnosing autoimmune diseases, cancer, infections (e.g.
 CC bacterial or viral) or inflammatory diseases, in transplantation
 CC therapies and for immunisation
 CC
 SQ Sequence 4 AA;
 Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 1
 1 GSY 3
 Db
 RESULT 12
 AAU84247
 ID AAU84247 standard; peptide; 4 AA.
 XX
 AC AAU84247;
 XX
 DT 08-MAY-2002 (first entry)
 DT
 XX
 DE Caspase cleavage site #11.
 XX
 KW Caspase; apoptosis; GAP SH3 binding protein; HCD2; AOP-1; cancer;
 KW apoptosis-associated disease; hyperproliferative disease; AIDS;
 KW degenerative disease; autoimmune disease; Alzheimer's disease;
 KW viral infection; acquired immunodeficiency syndrome; vascular disease;
 KW myocardial infarction; oxidative stress; ischaemic stroke; arthritis;
 KW heart failure; Parkinson's disease; amyotrophic lateral sclerosis.
 XX
 OS Unidentified.
 XX
 PN WO200196873-A2.
 PD
 XX 20-DEC-2001.
 PD
 XX 15-JUN-2001; 2001WO-EP006780.
 PF
 XX 16-JUN-2000; 2000EP-00112813.
 PR
 XX 16-NOV-2000; 2000EP-00125013.
 PR
 XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA
 XX Rudel T, Thiede B, Machny N;
 PI
 XX WPI; 2002-098088/13.
 XX
 XX Novel apoptosis-associated and/or -modified protein useful as target for
 PT the diagnosis, prevention or treatment of apoptosis-associated diseases
 PT particularly neurodegenerative diseases.
 PT
 XX Claim 30; Page 62; 86pp; English.
 XX
 XX The invention relates to an apoptosis-associated and/or -modified protein
 CC (I) selected from GAP SH3 binding protein, HCD2 and AOP-1 (not defined)
 CC or its proteolytic fragments. (I) is useful as target for the diagnosis,
 CC

CC prevention or treatment of apoptosis-associated diseases, for the
 CC manufacture of a pharmaceutical agent and for identifying apoptosis
 CC modulators. The proenzyme is useful as a target for the diagnosis,
 CC prevention or treatment of apoptosis-associated diseases, and in a method
 CC for identifying apoptosis modulators. (1) is useful for treatment of
 CC hyperproliferative or degenerative diseases including cancers, autoimmune
 CC diseases, Alzheimer's disease, viral infections such as acquired
 CC immunodeficiency syndrome (AIDS) and vascular diseases such as myocardial
 CC infarction. (1) is also useful for treating and/or preventing diseases
 CC related to oxidative stress like ischemic stroke, arthritis, heart
 CC failure, Parkinson's disease and amyotrophic lateral sclerosis. (1) is
 CC also useful for developing protein chip or other solid phase screening
 CC devices for high throughput screens, and also as a diagnostic tool to
 CC screen for caspase activity, and/or to determine the effectiveness of
 CC caspase cleavage inhibiting and/or modulating substances. AA084237-
 CC AA084260 represent caspase cleavage sites of the invention

SO Sequence 4 AA;

Query Match 86.7%; Score 13; DB 5; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 1 GSY 3

DB

RESULT 13
 AB018638

ID AB018638 standard; peptide; 4 AA.

AC AB018638;

DT 20-FEB-2003 (first entry)

DE ErbB receptor antagonist peptide #21.

KM Vaccine; erbB receptor antagonist; tumour; cancer; gastric cancer;
 KW breast cancer; prostate cancer.

OS Unidentified.

PN WO200281649-A2.

XX 17-OCT-2002.

PF 08-APR-2002; 2002WO-US011211.

PR 06-APR-2001; 2001US-0282037P.

PR 03-AUG-2001; 2001US-0309864P.

XX (TYPE-) UNIV PENNSYLVANIA.

PI Greene MI, Zhang H, Murali R, Richter M, Berezov A, Liu Q;

PI Chen J;

XX WPI; 2003-075482/07.

PT New peptide antagonists against erbB receptors, useful for preventing or
 PT treating tumors or cancers (e.g. lung adenocarcinomas, breast carcinomas
 PT or prostate cancer) in humans.

PS Claim 1; Page 82; 115pp; English.

CC The invention comprises peptide antagonists designed to target erbB
 CC receptors. The erbB receptor peptide antagonists are useful for
 CC preventing tumors and cancers (e.g. gastric cancer, breast cancer and
 CC prostate cancer). The present amino acid sequence represents an erbB
 CC receptor peptide antagonist of the invention

SO Sequence 4 AA;

Query Match 86.7%; Score 13; DB 6; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 2 GSY 4

DB

RESULT 14
 ABP59243

ID ABP59243 standard; peptide; 4 AA.

AC ABP59243;

DT 10-MAY-2003 (first entry)

DE Peptide epitope for generating cell surface receptor antibody, SEQ ID 21.

KM Antibody; cytostatic; vaccine; cell surface receptor; erbB; TNF;
 KW immunoglobulin gene superfamily; IgSF; epitope.

OS Synthetic.

PN WO2003012072-A2.

PD 13-FEB-2003.

PF 05-AUG-2002; 2002WO-US024892.

PR 03-AUG-2001; 2001US-0309864P.

XX (TYPE-) UNIV PENNSYLVANIA.

PI Greene MI, Zhang H, Richter M, Murali R;

PI WPI; 2003-268117/26.

PT Novel antibody for preventing, treating, imaging or diagnosing tumor, has
 PT specificity for activated cell surface receptor and binds specifically to
 PT an epitope that does not comprise phosphotyrosine residue.

PS Claim 53; Page 88; 114pp; English.

CC The present invention relates to novel antibodies, which have specificity
 CC for activated cell surface receptors (erbB, TNF and immunoglobulin gene
 CC superfamily: IgSF) and bind to an epitope (ABP59223-ABP59259). The
 CC antibodies are useful for preventing transformation of a normal cell into
 CC a tumour cell in a patient who had a tumour with tumour cells that
 CC express activated erbB receptors on the cell surface surgically removed
 CC or in whom the tumour has entered remission, for treating a patient
 CC suffering from a cancer characterised by tumour cells that have p185 on
 CC their cell surfaces, or for treating a patient suffering from an erbB
 CC tumour. The antibodies were produced by immunising a suitable host with a
 CC peptide (ABP59223-ABP59259), or its reverse sequence

SO Sequence 4 AA;

Query Match 86.7%; Score 13; DB 6; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
 2 GSY 4

DB

RESULT 15
 ADJ81984

ID ADJ81984 standard; peptide; 4 AA.

AC ADJ81984;

XX 06-MAY-2004 (first entry)
 DT Thermus brockianus nucleic acid polymerase peptide fragment #2.
 XX
 DE nucleic acid polymerase; thermophile; mutation; exonuclease activity.
 XX
 KW Thermus brockianus.
 XX
 OS WO2003048308-A2.
 XX
 PN 12-JUN-2003.
 XX
 PD 22-NOV-2002; 2002WO-US037657.
 XX
 PF 30-NOV-2001; 2001US-0334434P.
 XX
 PR (APPL-) APPLERA CORP.
 XX
 PI Rozzelle J, Bolchakova E;
 XX
 PI WPI; 2003-505285/47.
 DR
 XX
 XX
 PT New Thermus brockianus nucleic acid polymerases, useful for DNA
 PT synthesis, primer extension, DNA sequencing, reverse transcription, or
 PT DNA and RNA amplification procedures.
 XX
 PS Disclosure; SEQ ID NO 18; 74pp; English.
 XX
 CC The invention relates to novel nucleic acid polymerases from the
 CC thermophilic organism Thermus brockianus or mutants having a mutation
 CC that decreases 5'-'3' exonuclease activity or reduces discrimination
 CC against deoxynucleotide triphosphates. The nucleic acid polymerases,
 CC isolated nucleic acids encoding the polymerases, vectors, host cells and
 CC kits are useful for DNA synthesis, primer extension, DNA sequencing,
 CC reverse transcription, or DNA and RNA amplification procedures. The
 CC nucleic acids are also useful for the recombinant expression of the
 CC polymerase polypeptides. The nucleic acid polymerases and nucleic acids
 CC are useful for the detection and isolation of nucleic acids encoding DNA
 CC polymerase I activity. This sequence corresponds to a peptide of a
 CC polymerase of the invention.
 CC
 SQ Sequence 4 AA;

Query Match 86.7%; Score 13; DB 7; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 GXY 3
 |
 |
 Db 1 GAY 3

Search completed: December 13, 2004, 22:22:40
 Job time : 80 secs

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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:12:37 ; Search time 21.4 Seconds

(Without alignments)
12.396 Million cell updates/sec

Title: US-10-068-905-8

Perfect score: 15

Sequence: 1 GXYX 4

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*
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3: /cgn2_6/ptodata/1/1aa/5A COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/5B COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	86.7	4	1	US-08-798-897-49
2	13	86.7	4	1	US-08-463-224-2
3	13	86.7	4	2	US-08-463-377-2
4	13	86.7	4	2	US-08-978-923-49
5	13	86.7	4	2	US-08-310-912A-199
6	13	86.7	4	3	US-09-301-085-199
7	13	86.7	4	5	PCT-US93-01669-41
8	13	86.7	4	5	PCT-US95-04589-199
9	13	86.7	5	1	US-07-962-569A-6
10	13	86.7	5	2	US-08-292-968-30
11	13	86.7	5	2	US-08-292-968-30
12	13	86.7	5	2	US-08-618-696-3
13	13	86.7	5	2	US-08-618-696-14
14	13	86.7	5	2	US-08-467-974-30
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16	13	86.7	5	2	US-08-467-974-30
17	13	86.7	5	2	US-08-467-536-30
18	13	86.7	5	2	US-08-467-536-36
19	13	86.7	5	3	US-09-033-753-3
20	13	86.7	5	3	US-09-033-753-14
21	13	86.7	5	3	US-08-467-976-30
22	13	86.7	5	3	US-08-467-976-36
23	13	86.7	5	3	US-09-082-514-30
24	13	86.7	5	3	US-09-082-514-36
25	13	86.7	6	1	US-08-475-955-143
26	13	86.7	6	1	US-08-014-979-92
27	13	86.7	6	1	US-08-176-620A-21
			6	1	US-08-248-538-20

28	13	86.7	6	1	US-08-248-538-40	Sequence 40, Appl
29	13	86.7	6	1	US-08-260-199A-31	Sequence 31, Appl
30	13	86.7	6	1	US-08-260-199A-32	Sequence 32, Appl
31	13	86.7	6	1	US-08-798-897-53	Sequence 53, Appl
32	13	86.7	6	1	US-08-690-605-21	Sequence 21, Appl
33	13	86.7	6	2	US-08-580-988A-16	Sequence 16, Appl
34	13	86.7	6	2	US-08-461-985-21	Sequence 21, Appl
35	13	86.7	6	3	US-08-978-523-53	Sequence 53, Appl
36	13	86.7	6	3	US-08-481-985B-132	Sequence 132, App
37	13	86.7	6	3	US-08-932-787B-12	Sequence 12, Appl
38	13	86.7	6	3	US-08-932-012C-12	Sequence 12, Appl
39	13	86.7	6	3	US-08-888-818C-12	Sequence 12, Appl
40	13	86.7	6	4	US-09-518-737-6	Sequence 6, Appl
41	13	86.7	6	6	5200320-19	Sequence 12, Appl
42	13	86.7	7	1	US-07-841-997A-19	Patent No. 5200320
43	13	86.7	7	1	US-08-290-301-19	Sequence 19, Appl
44	13	86.7	7	2	US-09-070-756-8	Sequence 8, Appl
45	13	86.7	7	3	US-09-193-104-28	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-798-897-49
Sequence 49, Application US/08798897

Patent No. 5789201

GENERAL INFORMATION:

APPLICANT: Gaestlella, John

TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2

TITLE OF INVENTION: Homologue

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2540

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-798-897-49

Query Match 86.7%; Score 13; DB 1; Length 4;
Best Local Similarity 66.7%; Pred No. 3.8e+05; 1; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GAY 4

RESULT 2
US-08-463-224-2
Sequence 2, Application US/08463224
Patent No. 5807824
GENERAL INFORMATION:
APPLICANT: van Oostrom, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: Csa Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5807824agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,224
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-224-2
Query Match 86.7%; Score 13; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GXY 3
DB 2 GAY 4
RESULT 3
US-08-463-377-2
Sequence 2, Application US/08463377
Patent No. 5837499
GENERAL INFORMATION:
APPLICANT: van Oostrom, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: Csa Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5837499agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,377
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-377-2
Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GXY 3
DB 2 GAY 4
RESULT 4
US-08-978-523-49
Sequence 49, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Gastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483, 0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-978-523-49

Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 GXY 3
DB 2 GXY 4

RESULT 5
US-08-310-912A-199
Sequence 199, Application US/08310912A
Patent No. 5981730
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310-912A
FILING DATE: September 22, 1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/227,360
FILING DATE: April 13, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Iech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/254001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-310-912A-199

Query Match 86.7%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GXY 4

RESULT 6
US-09-301-085-199
Sequence 199, Application US/09301085
Patent No. 6262248
GENERAL INFORMATION:

APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.

APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
TITLE OF INVENTION: DETECTION METHODS
FILE REFERENCE: 00786/254002
CURRENT APPLICATION NUMBER: US/09/301,085
CURRENT FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: 08/310,912
EARLIER FILING DATE: 1994-09-22
EARLIER APPLICATION NUMBER: 08/227,360
EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 199
LENGTH: 4
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-301-085-199

Query Match 86.7%; Score 13; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GXY 4

RESULT 7
PCT-US93-01669-41
Sequence 41, Application PC/TUS9301669
GENERAL INFORMATION:
APPLICANT: Trombridge, Ian S.
APPLICANT: Collawn, Jr., James F.
APPLICANT: Tainer, John A.
APPLICANT: Kuhn, Leslie A.
TITLE OF INVENTION: RECEPTOR INTERNALIZATION SIGNALS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubae & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01669
FILING DATE: 01-MAR-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/844,852
FILING DATE: 03-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wechselt, Jr., Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1636
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US93-01669-41

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 2 GSY 4

RESULT 8
PCT-US95-04589-199
Sequence 199, Application PC/TUS9504589
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mandinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.303
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04589
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04589-199

Query Match 86.7%; Score 13; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 2 GTY 4

RESULT 9
US-07-962-569A-6
Sequence 6, Application US/07962569A
Patent No. 5381497
GENERAL INFORMATION:
APPLICANT: MENON, RAVI S.
APPLICANT: JEFFERS, KATHLEEN F.
APPLICANT: CHANG, YING-FON
APPLICANT: HAW, RICHARD G.
TITLE OF INVENTION: HUMAN K-CASEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FREDERICK W. PEPPER, PH.D.
STREET: 11545 W. BERNARDO COURT, STE. 302
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92127
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/962,569A
FILING DATE: 19921013
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 920224.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 451-1120
TELEFAX: (619) 451-9628
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-962-569A-6

Query Match 86.7%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 3 GTY 5

RESULT 10
US-08-292-968-30
Sequence 30, Application US/08292968
Patent No. 5856122
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: OOMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney

STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-388
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-968-30

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 5;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 11
US-08-292-968-36
Sequence 36, Application US/08292968
Patent No. 5856122
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COHEN, Raymond P.
APPLICANT: LOOSMORE, Sreeta
APPLICANT: KLEIN, Michael H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-388
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-968-36

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 5;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 2 GTY 4

RESULT 12
US-08-618-696-3
Sequence 3, Application US/08618696
Patent No. 5861475
GENERAL INFORMATION:
APPLICANT: COOPER, JR., J. ALLEN D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: INHIBITION OF PHAGOCYTES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,696
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,269
FILING DATE: 12/21/92
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 10AB-002/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acid residues
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-618-696-3

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 1 GAY 3

RESULT 13

US-08-618-696-14
Sequence 14; Application US/08618696
Patent No. 5861475

GENERAL INFORMATION:
APPLICANT: COOPER, J., J. ALLEN D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,696
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,269
FILING DATE: 12/21/92

ATTORNEY/AGENT INFORMATION:

NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UOAB:002/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7280
TELEFAX: 512-474-7577

TELEX: NOT APPLICABLE

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acid residues
TYPE: amino acid
STRANDEDNESS: single

US-08-618-696-14

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 1 GAY 3

RESULT 14

US-08-467-974-30
Sequence 30; Application US/08467974
Patent No. 5965385

GENERAL INFORMATION:

APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.

APPLICANT: COOPER, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michael H.
APPLICANT: ARMSTRONG, Glen D.
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESS: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,974
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/467,536

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/292,968

FILING DATE: 22-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,121

FILING DATE: 31-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/110,947

FILING DATE: 24-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: STEWART, Michael I.

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-454 MIS:V9

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single

US-08-467-974-30

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GTY 4

RESULT 15

US-08-467-974-36
Sequence 36; Application US/08467974
Patent No. 5965385

GENERAL INFORMATION:

APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COOPER, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michael H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46

Tue Dec 14 10:04:31 2004

us-10-068-905-8.rai

Page 7

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SIm & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,974
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,536
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/292,968
; FILING DATE: 22-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,121
; FILING DATE: 31-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/110,947
; FILING DATE: 24-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-454 MTS:V9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-974-36

Query Match 86.7%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GTY 4

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Job time : 21.4 secs

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Tue Dec 14 10:04:31 2004

us-10-068-905-8.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:31:47; Search time 68.6 Seconds
(without alignments)
20.827 Million cell updates/sec

Title: US-10-068-905-8
Perfect score: 15
Sequence: 1 GXYX 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA.*
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2: /cgn2_6/ptodate/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodate/2/pubpaa/US06_NEW_PUB.pep.*
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6: /cgn2_6/ptodate/2/pubpaa/PCTUS_PUBCOMB.pep.*
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17: /cgn2_6/ptodate/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodate/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodate/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodate/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	86.7	4	US-09-867-852-199	Sequence 199, App
2	13	86.7	4	US-10-302-817A-18	Sequence 18, App
3	13	86.7	4	US-10-613-472-199	Sequence 199, App
4	13	86.7	4	US-10-613-765-199	Sequence 199, App
5	13	86.7	5	US-09-792-686A-34	Sequence 34, App
6	13	86.7	5	US-10-344-779-8	Sequence 8, App
7	13	86.7	5	US-10-376-121A-143	Sequence 143, App
8	13	86.7	5	US-10-738-809-8	Sequence 8, App
9	13	86.7	5	US-10-394-471B-3	Sequence 3, App
10	13	86.7	5	US-10-394-471B-11	Sequence 11, App
11	13	86.7	6	US-09-990-762-36	Sequence 36, App
12	13	86.7	6	US-09-990-762-40	Sequence 40, App
13	13	86.7	6	US-09-990-762-41	Sequence 41, App

14	13	86.7	6	US-09-518-737-6	Sequence 6, App
15	13	86.7	6	US-09-858-852A-36	Sequence 36, App
16	13	86.7	6	US-09-858-852A-40	Sequence 40, App
17	13	86.7	6	US-09-858-852A-41	Sequence 41, App
18	13	86.7	6	US-10-285-045-23	Sequence 23, App
19	13	86.7	6	US-10-284-660-23	Sequence 23, App
20	13	86.7	6	US-10-394-980-232	Sequence 232, App
21	13	86.7	6	US-10-306-631-63	Sequence 63, App
22	13	86.7	6	US-10-435-751-108	Sequence 108, App
23	13	86.7	6	US-10-435-751-121	Sequence 121, App
24	13	86.7	6	US-10-133-234A-17	Sequence 17, App
25	13	86.7	6	US-10-133-234A-18	Sequence 18, App
26	13	86.7	6	US-10-133-234A-19	Sequence 19, App
27	13	86.7	6	US-10-133-234A-20	Sequence 20, App
28	13	86.7	6	US-10-133-234A-21	Sequence 21, App
29	13	86.7	6	US-10-415-014-732	Sequence 732, App
30	13	86.7	6	US-10-739-583-14	Sequence 14, App
31	13	86.7	6	US-10-813-638-1446	Sequence 1446, App
32	13	86.7	7	US-09-809-517A-15	Sequence 15, App
33	13	86.7	7	US-09-792-686A-31	Sequence 31, App
34	13	86.7	7	US-10-286-457-129	Sequence 129, App
35	13	86.7	7	US-10-286-457-189	Sequence 189, App
36	13	86.7	7	US-10-398-104-326	Sequence 326, App
37	13	86.7	7	US-10-741-481-35	Sequence 35, App
38	13	86.7	8	US-09-765-086-157	Sequence 157, App
39	13	86.7	8	US-09-756-283A-59	Sequence 59, App
40	13	86.7	8	US-09-756-283A-97	Sequence 97, App
41	13	86.7	8	US-09-962-445-15	Sequence 15, App
42	13	86.7	8	US-09-910-552-22	Sequence 22, App
43	13	86.7	8	US-09-880-748-3084	Sequence 3084, App
44	13	86.7	8	US-10-264-374-157	Sequence 157, App
45	13	86.7	8	US-10-375-992-157	Sequence 157, App

ALIGNMENTS

RESULT 1
US-09-867-852-199
Sequence 199, Application US/09867852
Patent No. US2002014732A1
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staekwitz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Funaki
APPLICANT: Mindrinos, Barbara N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
FILE REFERENCE: 00786/254002
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 09/301,085
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 199
LENGTH: 4
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-867-852-199
Query Match 86.7%; Score 13; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GTY 4

RESULT 2

US-10-302-817A-18
; Sequence 18, Application US/10302817A
; Publication No. US20030198978A1
; GENERAL INFORMATION:
; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAROVA, Elena
; TITLE OF INVENTION: THERMUS BROCKLIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768US
; CURRENT APPLICATION NUMBER: US/10/302,817A
; PRIOR FILING DATE: 2002-11-22
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Thermus brockianus
US-10-302-817A-18

Query Match 86.7%; Score 13; DB 14; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 1 GXY 3

RESULT 3

US-10-613-472-199
; Sequence 199, Application US/10613472
; Publication No. US20040088756A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumitaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254004
; CURRENT APPLICATION NUMBER: US/10/613,472
; PRIOR FILING DATE: 2003-07-02
; PRIOR FILING DATE: 2001-05-29
; PRIOR FILING DATE: 1999-04-28
; PRIOR FILING DATE: 1994-04-13
; PRIOR FILING DATE: 1994-09-22
; PRIOR FILING DATE: 1994-02-22
; PRIOR FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-472-199

Query Match 86.7%; Score 13; DB 15; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GTY 4

RESULT 4

US-10-613-765-199
; Sequence 199, Application US/10613765
; Publication No. US20040172673A1
; GENERAL INFORMATION:
; APPLICANT: AUSUBEL, FREDERICK M.
; APPLICANT: STASKAWICZ, BRIAN J.
; APPLICANT: KATAGIRI, FUMITAKI
; APPLICANT: KUNKEL, BARBARA N.
; APPLICANT: MINDRINOS, MICHAEL N.
; APPLICANT: YU, GUO-LIANG
; APPLICANT: BAKER, BARBARA
; APPLICANT: ELLIS, JEFFREY
; APPLICANT: SALMERON, JOHN
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254005
; CURRENT APPLICATION NUMBER: US/10/613,765
; PRIOR FILING DATE: 2003-07-02
; PRIOR FILING DATE: 2001-05-29
; PRIOR FILING DATE: 1999-04-28
; PRIOR FILING DATE: 1994-09-22
; PRIOR FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-765-199

Query Match 86.7%; Score 13; DB 16; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 2 GTY 4

RESULT 5

US-09-792-686A-34
; Sequence 34, Application US/09792686A
; Publication No. US20030068645A1
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Kopecky, Stephen L.
; APPLICANT: Meyand, Cornelia M.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR EVALUATING
; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
; FILE REFERENCE: 07039-250001
; CURRENT APPLICATION NUMBER: US/09/792,686A
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-686A-34

Query Match 86.7%; Score 13; DB 10; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Tue Dec 14 10:04:31 2004

us-10-068-905-8.rapb

Page 3

QY 1 GXY 3
Db 3 GTY 5

RESULT 6
US-10-344-779-8

; Sequence 8, Application US/10344779
; Publication No. US2003021106A1
; GENERAL INFORMATION:
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TORNETTA, MARK A.
; APPLICANT: TRUNEH, ALEMESEGED
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
; FILE REFERENCE: GP50033
; CURRENT APPLICATION NUMBER: US/10/344,779
; PRIOR FILING DATE: 2003-02-17
; PRIOR APPLICATION NUMBER: PCT/US01/26161
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,524
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/230,639
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-344-779-8

Query Match 86.7%; Score 13; DB 14; Length 5;
Best Local Similarity 66.7%; Pred. NO. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 1 GTY 3

RESULT 7
US-10-376-121A-143
; Sequence 143, Application US/10376121A
; Publication No. US2003021654A1
; GENERAL INFORMATION:
; APPLICANT: HARLEY, JOHN
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patricia L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: Apr:11 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991

APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMREF14CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 143:
US-10-376-121A-143

Query Match 86.7%; Score 13; DB 14; Length 5;
Best Local Similarity 66.7%; Pred. NO. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 1 GTY 3

RESULT 8
US-10-738-809-8
; Sequence 8, Application US/10738809
; Publication No. US2004017117A1
; GENERAL INFORMATION:
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TORNETTA, MARK A.
; APPLICANT: TRUNEH, ALEMESEGED
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
; FILE REFERENCE: GP50033
; CURRENT APPLICATION NUMBER: US/10/738,809
; CURRENT FILING DATE: 2003-12-17
; PRIOR APPLICATION NUMBER: US/10/344,779
; PRIOR FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: PCT/US01/26161
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,524
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/230,639
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-738-809-8

Query Match 86.7%; Score 13; DB 16; Length 5;
Best Local Similarity 66.7%; Pred. NO. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
Db 1 GTY 3

RESULT 9
US-10-394-471B-3
; Sequence 3, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
; APPLICANT: GILES-KOMAR, JILL; CARTON, JILL; SCALLON, BERNARD J.

```

; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0202
; CURRENT APPLICATION NUMBER: US/10/394,471B
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/367,903
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver 3.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-471B-3

Query Match
Best Local Similarity 86.7%; Score 13; DB 16; Length 5;
Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 2 GSY 4

RESULT 10
US-10-394-471B-11
; Sequence 11, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill; Carton, Jill; Scallion, Bernard J.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0202
; CURRENT APPLICATION NUMBER: US/10/394,471B
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/367,903
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver 3.1
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-471B-11

Query Match
Best Local Similarity 86.7%; Score 13; DB 16; Length 5;
Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 2 GSY 4

RESULT 11
US-09-990-762-36
; Sequence 36, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 36
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-990-762-36

Query Match
Best Local Similarity 86.7%; Score 13; DB 9; Length 6;
Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
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Db 3 GAY 5

RESULT 12
US-09-990-762-40
; Sequence 40, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
; OTHER INFORMATION: recognition sequence
US-09-990-762-40

Query Match
Best Local Similarity 86.7%; Score 13; DB 9; Length 6;
Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 3 GAY 5

RESULT 13
US-09-990-762-41
; Sequence 41, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
OTHER INFORMATION: recognition sequence
US-09-990-762-41

Query Match
Best Local Similarity 86.7%; Score 13; DB 9; Length 6;
Matches 2; Conservative 0; Pred. No. 1.4e+06;
Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
3 GAY 5

Db

RESULT 14
US-09-518-737-6
Sequence 6, Application US/09518737
Publication No. US20030008321A1
GENERAL INFORMATION:
APPLICANT: FUKUI, YASUHIISA
APPLICANT: NAGATA, SATOSHI
APPLICANT: SHIRAI, RYUICHI
APPLICANT: SAITO, NAOAKI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
FILE REFERENCE: 1965/49618
CURRENT APPLICATION NUMBER: US/09/518.737
CURRENT FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: JP 1999-250209
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 6
TYPE: PRT
ORGANISM: Mus musculus
US-09-518-737-6

Query Match
Best Local Similarity 86.7%; Score 13; DB 10; Length 6;
Matches 2; Conservative 0; Pred. No. 1.4e+06;
Mismatches 1; Indels 0; Gaps 0;

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4 GSY 6

Db

RESULT 15
US-09-858-852A-36
Sequence 36, Application US/09858852A
Publication No. US20030044787A1
GENERAL INFORMATION:
APPLICANT: JOUNG, J. KEITH
APPLICANT: MILLER, JEFFREY
APPLICANT: PABO, CARL O.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
FILE REFERENCE: MTV-030.01 (20021-3001)
CURRENT APPLICATION NUMBER: US/09/858.852A
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/204,509
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
OTHER INFORMATION: recognition sequence
US-09-858-852A-36

Query Match 86.7%; Score 13; DB 10; Length 6;

Best Local Similarity 86.7%; Score 13; DB 9; Length 6;
Matches 2; Conservative 0; Pred. No. 1.4e+06;
Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
3 GAY 5

Db

Search completed: December 13, 2004, 23:02:40
Job time : 68.6 secs

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GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: December 13, 2004, 22:01:21 ; Search time 15.2 Seconds
(without alignments)
25.320 Million cell updates/sec

Title: US-10-068-905-8
Perfect score: 15
Sequence: 1 GXYX 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	13	86.7	9 2	Ig heavy chain V r
3	13	86.7	11 2	T-cell receptor ga
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5	13	86.7	12 2	T-cell receptor be
6	13	86.7	12 2	163k exoantigen -
7	13	86.7	12 2	T-cell antigen rec
8	13	86.7	12 2	Ig H chain V-D-U r
9	13	86.7	12 2	T-cell receptor al
10	13	86.7	12 2	PH0790
11	13	86.7	13 2	S47368
12	13	86.7	13 2	S47383
13	13	86.7	13 2	PH0788
14	13	86.7	13 2	PQ0700
15	13	86.7	14 2	AS9018
16	13	86.7	14 2	PH1601
17	13	86.7	14 2	PH0792
18	13	86.7	15 2	PH1582
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20	13	86.7	17 2	S48655
21	13	86.7	17 2	AG0317
22	13	86.7	17 2	P35141
23	13	86.7	18 2	I73024
24	13	86.7	18 2	PH1529
25	13	86.7	19 2	PH1609
26	13	86.7	20 2	PH1609
27	13	86.7	20 2	CA0142
28	13	86.7	20 2	AS4519
29	13	86.7	20 2	PL0161

30	13	86.7	20 2	S44465	pyrrocoricin - Py
31	13	86.7	21 2	PT0227	Ig heavy chain CDR
32	13	86.7	21 2	S47198	T-cell receptor U-
33	13	86.7	21 2	S47212	T-cell receptor U-
34	13	86.7	22 2	PH1680	Ig heavy chain V r
35	13	86.7	22 2	A53794	tyrocidine synthas
36	13	86.7	23 2	A53631	H+-transporting tw
37	13	86.7	23 2	PH1725	Ig heavy chain V r
38	13	86.7	24 2	I73584	alpha 1-proteinase
39	13	86.7	24 2	I61491	seed protein ws-9
40	13	86.7	24 2	D27579	T-cell receptor be
41	13	86.7	24 2	A05298	fibrinogen gamma c
42	13	86.7	24 2	E45087	cysteine proteinas
43	13	86.7	24 2	S56000	guanine kinase M
44	13	86.7	25 2	A58647	alpha-conotoxin p
45	13	86.7	26 2	PQ0105	alkaline serine pr

ALIGNMENTS

RESULT 1
S36850
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1995
C/Accession: S36850
R/Jacob, J.; Kelsoe, G.
Submitted to the EMBL Data Library, July 1992
A/Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophen
A/Reference number: S25024
A/Accession: S36850
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-9 <UAC>
A/Cross-references: EMBL:X67387; NID:S50113; PIDN:CAA47799.1; PID:S51594; PID:g1333871
C/Keywords: heterotetramer; immunoglobulin

Query Match 86.7% ; Score 13; DB 2; Length 9;
Best local similarity 66.7% ; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 6 GSY 8

RESULT 2
G41946
T-cell receptor gamma chain (2t.23) - mouse (fragment)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1995
C/Species: Mus musculus (house mouse)
C/Accession: G41946
R/Whetzel, M.; Mosley, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A/Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A/Reference number: A41946; MUID:92049316; PMID:1658619
A/Accession: G41946
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-9 <WHB>
C/Keywords: T-cell receptor

Query Match 86.7% ; Score 13; DB 2; Length 9;
Best local similarity 66.7% ; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GSY 5

RESULT 3

PT0250
IG heavy chain CRD3 region (clone 2-109B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0250
R/Amada, M.; Hasserman, R.; Reichard, B.A.; Shane, S.; Cator, A.J.; Rovera, G.
U. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0250
A/Molecule type: DNA
A/Residues: 1-11 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterocyclamer; immunoglobulin

Query Match 86.7%; Score 13; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 8.1e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 1 GXY 3

RESULT 4
PT0214
T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C/Accession: PT0214
R/Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
U. Exp. Med. 173, 1091-1097, 1991
A/Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted
A/Reference number: PT0209; MUID:91217621; PMID:1902501
A/Accession: PT0214
A/Molecule type: mRNA
A/Residues: 1-11 <YAK>
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 8.1e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 5 GXY 7

RESULT 5
A33099
163K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C/Species: Plasmodium falciparum
C/Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C/Accession: A33099
R/Nichols, J.H.; Hager, L.P.
Submitted to the Protein Sequence Database, May 1990
A/Reference number: A33098
A/Accession: A33099
A/Status: Preliminary
A/Molecule type: Protein
A/Residues: 1-12 <NIC>

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 9 GXY 11

RESULT 6
S47391

T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47391, S47386
R/Heimer, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A/Reference number: S47355
A/Accession: S47391
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <LEH>
A/Cross-references: EMBL:Z35712; NID:9527519; PIDD:CAA84784.1; PID:9527520; EMBL:Z3570
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 6 GXY 8

RESULT 7
S47395
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47395
R/Heimer, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A/Reference number: S47355
A/Accession: S47395
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <LEH>
A/Cross-references: EMBL:Z35715; NID:9527525; PIDD:CAA84784.1; PID:9527526
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 6 GXY 8

RESULT 8
PH1611
Ig H chain V-D-J region (wild-type clone 341) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1611
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
U. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A/Reference number: PH1580; MUID:93301609; PMID:8315387
A/Accession: PH1611
A/Molecule type: DNA
A/Residues: 1-12 <LEV>
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
| |
Db 5 GXY 7

RESULT 9

PH0802
T-cell receptor alpha chain (M2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0802
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0802
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X60910
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 6 GTY 8

RESULT 10

PH0790
T-cell receptor alpha chain (Q37.3.2 V-alpha-4.3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0790
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0790
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X60895
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 6 GTY 8

RESULT 11

S47368
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47368
R/Lehner, P.U.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by T
A/Reference number: S47355
A/Accession: S47368
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:Z35693; NID:9527477; PIDN:CAA84762.1; PID:9527478
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 7 GTY 9

RESULT 12

S47383
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47383
R/Lehner, P.U.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by T
A/Reference number: S47355
A/Accession: S47383
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:Z35709; NID:9527513; PIDN:CAA84778.1; PID:9527514
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 7 GTY 9

RESULT 13

PH0788
T-cell receptor alpha chain (E22 V-alpha-8.F3.4) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0788
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0788
A/Molecule type: mRNA
A/Residues: 1-13 <CAS>
A/Cross-references: EMBL:X60893
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 7 GTY 9

RESULT 14

P00700
unidentified 6.3/40K protein [imported] - rice (fragment)
C/Species: Oryza sativa (rice)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: P00700
R/Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A/Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A/Reference number: F00696
A/Accession: P00700

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <KOM>
A:Cross-references: UNIPROT:Q7M1U1

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 3 GAY 5

RESULT 15

A59018
MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
C:Accession: A59018
R:Abel, M.; Smith, C.J.; Larson, C.J.
submitted to the Protein Sequence Database, May 1998
A:Description: Involvement of "Xu-like" proteins in the transcription of MUC1/DF3, a breast cancer cell line MCF-7
A:Reference number: A59018
A:Accession: A59018
A:Molecule type: protein
A:Residues: 1-14 <ABE>
A:Experimental source: breast cancer cell line MCF-7
A>Note: 3-Val was also found
C:Keywords: DNA binding; heterodimer

Query Match 86.7%; Score 13; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
| |
Db 6 GSY 8

Search completed: December 13, 2004, 22:32:59
Job time : 15.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:00:41; Search time 83.8 seconds
(without alignments)
27.464 Million cell updates/sec

Title: US-10-068-905-8
Perfect score: 15
Sequence: 1 GXVX 4

Scoring table: ELOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	86.7	8	1	UP06_MOUSE
2	13	86.7	9	2	Q9QWTO
3	13	86.7	10	2	Q8NBY9
4	13	86.7	10	2	AA063472
5	13	86.7	11	2	Q9UC46
6	13	86.7	11	2	Q7YF62
7	13	86.7	13	1	ADFB_TENMO
8	13	86.7	13	1	P82432
9	13	86.7	13	2	Q7YF62
10	13	86.7	13	2	Q7YF62
11	13	86.7	15	1	PH3_PROUSE
12	13	86.7	15	1	UC14_MAIZE
13	13	86.7	15	2	Q47892
14	13	86.7	15	2	Q47892
15	13	86.7	15	2	Q47892
16	13	86.7	16	1	PH2_PROUSE
17	13	86.7	16	2	Q7IGD2
18	13	86.7	16	2	Q6JDK5
19	13	86.7	16	2	Q6JDK5
20	13	86.7	17	2	Q6JDK5
21	13	86.7	17	2	Q6JDK5
22	13	86.7	17	2	Q6JDK5
23	13	86.7	17	2	Q6JDK5
24	13	86.7	17	2	Q6JDK5
25	13	86.7	17	2	Q6JDK5
26	13	86.7	17	2	Q6JDK5
27	13	86.7	17	2	Q6JDK5
28	13	86.7	17	2	Q6JDK5
29	13	86.7	18	2	Q6JDK5
30	13	86.7	18	2	Q6JDK5
31	13	86.7	18	2	Q6JDK5

32	13	86.7	18	2	Q9R4C6	Q9R4C6 agrobacteri
33	13	86.7	18	2	Q9R4F9	Q9R4F9 aeromonas
34	13	86.7	18	2	Q9R501	Q9R501 bacillus su
35	13	86.7	18	2	Q9R501	Q9R501 bacillus su
36	13	86.7	18	2	Q9R501	Q9R501 bacillus su
37	13	86.7	18	2	Q9R501	Q9R501 bacillus su
38	13	86.7	18	2	Q9R501	Q9R501 bacillus su
39	13	86.7	18	2	Q9R501	Q9R501 bacillus su
40	13	86.7	18	2	Q9R501	Q9R501 bacillus su
41	13	86.7	18	2	Q9R501	Q9R501 bacillus su
42	13	86.7	18	2	Q9R501	Q9R501 bacillus su
43	13	86.7	18	2	Q9R501	Q9R501 bacillus su
44	13	86.7	18	2	Q9R501	Q9R501 bacillus su
45	13	86.7	18	2	Q9R501	Q9R501 bacillus su

ALIGNMENTS

RESULT 1	ID	UP06_MOUSE	STANDARD	PRT	8 AA
AC	P38644				
DT	01-OCT-1994	(Rel. 30, Created)			
DT	01-OCT-1994	(Rel. 30, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DE	Unknown protein from 2D-PAGE of fibroblasts (P50) (fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RP	SEQUENCE				
RC	TISSUE=Fibroblast;				
RX	MEDLINE=9509907; PubMed=7523108;				
RA	Wierick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.,				
RT	"Separation and sequencing of familial and novel murine proteins using				
RL	preparative two-dimensional gel electrophoresis."				
CC	Electrophoresis 15:735-745(1994).				
CC	-1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown				
CC	protein is: 5.2. Its MW is: 50 KDa.				
KM	Direct protein sequencing.				
PT	NON-TER				
SQ	SEQUENCE 8 AA; 817 MW; A35DB87676B05B1 CRC64;				
Query Match					
Best Local Similarity	86.7%; Score 13; DB 1; Length 8;				
Matches	2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
DB	1 GXV 3				
	6 GAV 8				
RESULT 2					
ID	Q9QWTO	PRELIMINARY;	PRT;	9 AA.	
AC	Q9QWTO				
DT	01-MAY-2000	(TREMblrel. 13, Created)			
DT	01-MAY-2000	(TREMblrel. 13, Last sequence update)			
DE	Proteinase 3 (Myeloblastin) (fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=SV129 D3;				
RA	Lutz P.G., Moez-Lutz C., Houzel-Charavel A., Cayre Y.E.;				
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBD databases.				
DR	EMBL; AJ007030; CAA07429.1; -				

DR MCD, MG1:893580; PRTn3.
FT NON_TER 9
SQ SEQUENCE 9 AA; 937 MW; C91E75A77B45B87D CRC64;

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 9;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GSY 5

RESULT 3
Q8NEB9 PRELIMINARY; PRT; 10 AA.

AC Q8NEB9; 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Type II hair-specific keratin (Type II hair keratin) (Fragment).
GN Name=KRTHB6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Baitwa N.K., Bamezai R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
R2 (2)
RP SEQUENCE FROM N.A.
RA Baitwa N.K., Bamezai R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039552; AAK6868.1;
DR EMBL; AY039552; AAK6868.1;
DR GO; GO:0005882; C:intermediate filament; IEA.
KW Keratin.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1034 MW; 9B53417EAB45B87E CRC64;

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 10;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GSY 6

RESULT 4
AA063472 PRELIMINARY; PRT; 10 AA.
AC AA063472;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Type II hair keratin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Baitwa N.K., Bamezai R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039552; AAK6868.1;
DR EMBL; AY039552; AAK6868.1;
DR GO; GO:0005882; C:intermediate filament; IEA.
KW Keratin.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1034 MW; 9B53417EAB45B87E CRC64;

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GSY 6

RESULT 5
Q9UC46 PRELIMINARY; PRT; 11 AA.

AC Q9UC46; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Neutrophil inhibitor peptide, NIP-POLYMORPHON/CLEAR neutrophil
DE inhibitor peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE.
RX MEDLINE=96326114; PubMed=8703476;
RA Cooper J.A., Jr., Culbreth R.R.;
RT "Characterization of a neutrophil inhibitor peptide harvested from
RT human bronchial lavage: homology to influenza A nucleoprotein.";
RL Am. J. Respir. Cell Mol. Biol. 15:207-215(1996).
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0030236; P:anti-inflammatory response; NAS.
SQ SEQUENCE 11 AA; 1262 MW; 951A1C3279C9DB45 CRC64;

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 11;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GSY 5

RESULT 6
Q7YP62 PRELIMINARY; PRT; 11 AA.
AC Q7YP62; 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MHC class Ib antigen (Fragment).
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Liu Y., He X., Xu L., Zeng Y.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY328516; AAP94210.1;
DR EMBL; AY328516; AAP94210.1;
FT NON_TER 1
SQ SEQUENCE 11 AA; 1208 MW; 2E0B6C5C5A845B8 CRC64;

Query Match
Best Local Similarity 86.7%; Score 13; DB 2; Length 11;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GSY 6

RESULT 7
ADFB_TENMO

ID ADFB TENMO STANDARD; PRT; 13 AA.
AC P83109;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-UTL-2004 (Rel. 44, Last annotation update)
DE Antidiuretic factor B (ADFB)
OS Tenebrio molitor (Yellow mealworm)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
RP SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=22465067; PubMed=12576082;
RA Eighmeier R.A., Wiehart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,
Hull J.J., Schooley D.A.;
RT "Isolation, identification and localization of a second beetle
antidiuretic peptide";
RU Peptides 24(2):34(2003).
CC -1- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses
CC CGMP as second messenger. May function as an antidiuretic hormone.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two
CC pairs of bilaterally symmetrical cells in the protocerebrum.
CC -1- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI; RANGE=1-13;
CC NOT-Ref.1.
KW Direct protein sequencing; Hormone; Neuropeptide.
SQ SEQUENCE 13 AA; 1562 MW; 0240A504B8A633B CRC64;

Query Match 86.7%; Score 13; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 4 GAY 6

RESULT 8
P82432 PRELIMINARY; PRT; 13 AA.
AC P82432;
DT 01-JUN-2000 (TRENBLREL. 14, Created)
DT 01-JUN-2000 (TRENBLREL. 14, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE 31 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
Wojtasek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
tobacco cultures";
RU Planta 010-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON TER
SQ SEQUENCE 13 AA; 1307 MW; D5022297D8697DC6 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3

DB 9 GAY 11

RESULT 9
Q7M1U1 PRELIMINARY; PRT; 13 AA.
AC Q7M1U1;
DT 01-MAR-2004 (TRENBLREL. 26, Created)
DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Unidentified 63/40K protein (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA Komatsu S., Kajiwara H., Hirano H.;
RT "A rice protein library; a data-file of rice proteins separated by
RT two-dimensional electrophoresis";
RL Theor. Appl. Genet. 86:935-942(1993).
DR PIR; PQ0700; PQ0700.
FT NON TER
FT NON TER
SQ SEQUENCE 13 AA; 1218 MW; 27EA7291E7D3D878 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 3 GAY 5

RESULT 10
Q7YOR1 PRELIMINARY; PRT; 13 AA.
AC Q7YOR1;
DT 01-OCT-2003 (TRENBLREL. 25, Created)
DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Gamma-glutamylcysteine synthetase (EC 6.3.2.2) (Fragment).
GN Name-gsh1;
OS Brassica juncea (leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euraeid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RP SEQUENCE FROM N.A.
RA Wächter A., Steininger H., Rausch T., Bogs U.;
RL Submitted (MAY-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ564376; CAD91995.1;
DR GO; GO:0004357; F:glutamate-cysteine ligase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
KW Ligase.
FT NON TER
SQ SEQUENCE 13 AA; 1266 MW; DBF2097182417DC6 CRC64;

Query Match 86.7%; Score 13; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GXY 3
DB 9 GAY 11

RESULT 11
PH3_PRUS8

ID PH3 PRUSE STANDARD; PRT; 15 AA.
 AC P23265;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Prunasin beta-glucosidase IIB (BC 3.2.1.118) (Prunasin hydrolase isozyme IIB) (PH IIB) (Fragment).
 OS Prunus serotina (Black cherry).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC Eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 NCBI_TaxID=23207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RA Li C.P., Swain E., Poulton J.E.;
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase."; Plant Physiol. 100:282-290 (1992).
 RL -1- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-glucose.
 CC -1- SUBUNIT: Monomer.
 CC -1- DEVELOPMENTAL STAGE: Absent from maturing black cherry fruits until 6 weeks after flowering. Then, concomitant with cotyledon development, the level of enzyme increases with specificity for embryonal tissues.
 CC -1- PTM: Glycosylated.
 CC Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
 KW Multigene family.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1635 MW; 4F3D7F4FB90CFE4C CRC64;
 Query Match 86.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CY 1 GXY 3
 DB 1 GTY 3
 RESULT 12
 UC14 MAIZE STANDARD; PRT; 15 AA.
 ID UC14 MAIZE
 AC P80620;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 258) (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C., Pernelle J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated genome analysis program." Theor. Appl. Genet. 93:997-1005 (1996).
 RL -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 5.9, its MW is: 34.6 kDa.
 CC Maize-2DPAGE; P80620; COLEOPTILE.
 DR MaizeDB; 123944;
 KW Direct protein sequencing.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1564 MW; CFOBBA0B7DE658 CRC64;
 Query Match 86.7%; Score 13; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CY 1 GXY 3
 DB 7 GAY 9
 RESULT 13
 ID 0958L4 PRELIMINARY; PRT; 15 AA.
 AC 0958L4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-D-glucoside glucosylase (EC 3.2.1.21) (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=94347094; PubMed=8068000;
 RA Feldwisch J., Vente A., Zetl R., Bako L., Campos N., Palme K.;
 RT "Characterization of two membrane-associated beta-glucosidases from RT maize (Zea mays L.) coleoptiles." Biochem. J. 302:15-21 (1994).
 RL Biochem. J. 302:15-21 (1994).
 DR GO: GO:0008422; Fibeta-glucosidase activity; IBA.
 SQ SEQUENCE 15 AA; 1667 MW; 46C40370DC6C730B CRC64;
 Query Match 86.7%; Score 13; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CY 1 GXY 3
 DB 3 GST 5
 RESULT 14
 ID 047892 PRELIMINARY; PRT; 15 AA.
 AC 047892;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-allophycocyanin (Fragment).
 OS Fremyella diplosiphon (Calochrix PCC 7601).
 OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
 NCBI_TaxID=1197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66233345; PubMed=3086870;
 RA Conley P.B., Lemaux P.G., Lomax T.L., Grossman A.R.;
 RT "Genes encoding major light-harvesting polypeptides are clustered on RT the genome of the cyanobacterium Fremyella diplosiphon." J. Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928 (1986).
 DR EMBL; M13216; AAA24871.1;
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1644 MW; 9727165699F462F CRC64;
 Query Match 86.7%; Score 13; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CY 1 GXY 3
 DB 4 GST 6
 RESULT 15
 ID 047893 PRELIMINARY; PRT; 15 AA.
 ID 047893

AC 047893;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Beta-phycocyanin (Fragment).
 OS Fremyella diplosiphon (Calothrix PCC 7601).
 OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
 NCBI_TaxId=1197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86233345; PubMed=3086870;
 RA Conley P.B., Lemaux P.G., Lemaux T.L., Grossman A.R.;
 RT "Genes encoding major light-harvesting polypeptides are clustered on
 the genome of the cyanobacterium Fremyella diplosiphon.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928(1986).
 DR EMBL; M1321; AAA24880.1; -
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1528 MM; 7FF2F65518F493D4 CRC64;
 Query Match 86.7%; Score 13; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GXY 3
 Db 4 GSY 6

Search completed: December 13, 2004, 22:31:37
 Job time : 83.8 secs

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PS Claim 7, Page 83; 103pp; English.

CC The invention relates to a group of linear or cyclic tetra- to deca-peptides which include Peptide T and its analogues, where at least one of the amino acids may optionally have a monomeric or polymeric carbohydrate substituted onto a hydroxyl, amino and/or amide group. In one aspect the invention relates to the use of these peptides for the treatment of inflammation; and in another aspect it relates to those peptides in which the carbohydrate moiety is present (other than glycosylated prototype Peptide T) as new chemical entities. The present peptide is one of 10 specific peptides listed in a sub-claim for use in the treatment of inflammation. The peptides act as immunomodulators in the treatment and prevention of inflammation. In particular they can be used in the treatment of multiple sclerosis, myopathies (including HIV-1 associated myopathies) and symptoms and diseases associated with chronic immune activation including chronic fatigue syndrome, toxic shock, arthritis, inflammatory bowel disease, and host-versus-graft and graft-versus-host responses in transplant recipients. (Updated on 25-MAR-2003 to correct PN field.)

CC Sequence 4 AA;

SO Query Match 85.7%; Score 12; DB 2; Length 4; Best Local Similarity 66.7%; Pred. No. 1.7e+06; Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTY 3
1 TTY 3

DB

RESULT 2
ID AAR59492 standard; peptide; 4 AA.
AC AAR59492;
XX
DT 25-MAR-2003 (revised)
DT 26-NOV-1995 (first entry)
XX
DE Peptide T variant used for treating eczema.
XX
KM peptide T; prototype; octapeptide; eczema; dermatitis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT
XX
PN WO9508338-A1.
XX
PD 30-MAR-1995.
XX
PF 26-SEP-1994; 94WO-AU000574.
XX
PR 24-SEP-1993; 93AU-00001449.
XX
PA (PEPT-) PEPTIDE TECHNOLOGY LTD.
XX
PI Michaelis J, Trigg TE;
XX
DR WPI; 1995-139385/18.
XX
PT Treatment or prevention of eczema or dermatitis, esp. atopic eczema - using specified peptide, e.g the octapeptide Peptide T.
XX
PS Claim 3; Page 15; 20pp; English.
XX
CC The invention relates to a new method of treating eczema or dermatitis using Peptide T and its variants. The present sequence represents one of

CC the preferred variants. (Updated on 25-MAR-2003 to correct PN field.)

SO Sequence 4 AA;

QY 1 TTY 3
1 TTY 3

DB

RESULT 3
ID AAR61487 standard; peptide; 4 AA.
AC AAR61487;
XX
DT 25-MAR-2003 (revised)
DT 26-NOV-1995 (first entry)
XX
DE Peptide T variant for use in treating Crohn's disease.
XX
KM peptide T; prototype; octapeptide; Crohn's disease; ulcerative; colitis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT
XX
PN WO9508339-A1.
XX
PD 30-MAR-1995.
XX
PF 26-SEP-1994; 94WO-AU000575.
XX
PR 24-SEP-1993; 93AU-00001448.
XX
PA (PEPT-) PEPTIDE TECHNOLOGY LTD.
XX
PI Michaelis J, Sleight MJ;
XX
DR WPI; 1995-139386/18.
XX
PT Treatment or prevention of Crohn's disease or ulcerative colitis - by use of specified peptide, e.g. Peptide T.
XX
PS Claim 3; Page 15; 24pp; English.
XX
CC The invention relates to a new method of treating or preventing Crohn's disease and/or ulcerative colitis using Peptide T and its variants. The present sequence is one of the preferred peptides. (Updated on 25-MAR-2003 to correct PN field.)

SO Sequence 4 AA;

QY 1 TTY 3
1 TTY 3

DB

RESULT 4
ID AAB24318 standard; peptide; 4 AA.
XX

AC AAB24318;
XX
XX 13-FEB-2001 (first entry)
XX
DE Human H38087 casein kinase II phosphorylation site peptide SEQ ID NO:53.
XX
XX Human; prostate tumour associated gene; 24P4C12; prostate cancer;
XX transmembrane protein; diagnosis; anticancer; cytostatic; vaccine;
XX gene therapy.
XX Homo sapiens.
XX
XX WO200061746-A1.
XX
XX 19-OCT-2000.
XX
XX 12-APR-2000; 2000WO-US010039.
XX
XX 12-APR-1999; 99US-0128558P.
XX
XX (UDOG-) UROGENESIS INC.
XX
XX Afar DE, Hubert RS, Leong K, Raitano AB, Saffran DC;
XX WPI; 2000-672681/65.
XX
XX Novel 24P4C12 polypeptides and polynucleotides, used in the diagnosis and
XX treatment of cancer, especially prostate cancer.
XX
XX Disclosure; Page 35; 137pp; English.
XX
XX The present invention describes a prostate tumour associated gene,
XX designated 24P4C12, and its encoded protein. 24P4C12 has anticancer and
XX cytostatic activity, and can be used in vaccine production and in gene
XX therapy. A pharmaceutical composition or vaccine comprising 24P4C12 can
XX be used to treat a patient with cancer, especially prostate cancer, the
XX vaccine can also be used to inhibit the development or progression of
XX cancer. The polypeptides and polynucleotides can be used to diagnose
XX cancers, especially prostate cancer. A transgenic animal comprising
XX 24P4C12 can be used for the development and screening of therapeutic
XX reagents. The polypeptide is a transmembrane protein which is expressed
XX specifically in prostate cancer, allowing the development of more
XX specific anticancer therapies and diagnostic assays.
XX
XX Sequence 4 AA;
SQ
Query Match 85.7%; Score 12; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TXY 3
DB 1 TTY 3
RESULT 5
AAB05432
ID AAB05432 standard; peptide; 4 AA.
XX
XX AAB05432;
XX
XX 24-OCT-2001 (first entry)
XX
XX Synthetic tetrapeptide ligand 14.
XX
XX Terapeptide ligand; drug design; high throughput screening; HTS; MGSAR;
XX Multivariate Quantitative Structure Activity relationships.
XX
XX Synthetic.
XX
XX WO200136980-A2.
XX
XX 25-MAY-2001.
XX
XX PD

XX
XX 20-NOV-2000; 2000WO-GB004420.
XX
XX 18-NOV-1999; 99GB-00027346.
XX
XX (MELA-) MELACRE THERAPEUTICS AB.
XX
XX (PETT/) PETT C P.
XX
XX Lundstedt T, Andersson P, Wikberg J, Muceniece R, Prusis P;
XX WPI; 2001-432565/46.
XX
XX A novel method for identifying the interaction site, binding site or
XX active site in a macromolecule, using of informative combinatorial
XX chemistry, informative peptide libraries and Multivariate Quantitative
XX Structure Activity Relationships.
XX
XX Example 5; Fig 27; 131pp; English.
XX
XX The sequence represents a tetrapeptide ligand selected according to 2 (12
XX -7) fractional factorial design +3 cp (or 1 cp 2 random), which were used
XX to model the interaction of a ligand with its target. The invention
XX relates to characterizing the interaction between a ligand Y and a Target
XX X by obtaining information (e.g. Multivariate Quantitative Structure
XX Activity relationships, MGSAR) representing one or more physical and/or
XX chemical properties of targets of type X and type Y to produce a model of
XX interaction. The methods of the invention are useful for identifying
XX outliers of type X or outliers of type Y, drug design, design or
XX identification of lead compounds (e.g. by high throughput screening, HTS),
XX design of ligands of type Y with improved affinity and/or selectivity for
XX targets of type X, protein engineering, design of DNA or RNA molecules,
XX design of artificial targets of type X/or artificial ligands of type Y,
XX analysis and/or in the engineering of regions and/or parts of targets of
XX type X and/or ligands of type Y, design of organic compound, catalyst,
XX pharmaceutical, drug, macromolecule being capable of binding a molecule,
XX peptidomimetic, protein, enzyme, antibody, molecule, macromolecule, DNA,
XX RNA or a carbohydrate. The methods are also useful for designing new
XX ligands for known targets and/or for new targets
XX
XX Sequence 4 AA;
SQ
Query Match 85.7%; Score 12; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TXY 3
DB 2 TTY 4
RESULT 6
ABG61618
ID ABG61618 standard; peptide; 4 AA.
XX
XX ABG61618;
XX
XX 12-AUG-2002 (first entry)
XX
XX Tetrapeptide amide inhibitor #3 used to inhibit DPPIV activity.
XX
XX Human; serine protease; dipeptidyl peptidase IV-related protein, DPPIV;
XX DPPIV; infection; human immunodeficiency virus; HIV-1, HIV-2; pain;
XX diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
XX heart failure; hypertension; urinary retention; osteoporosis; cancer;
XX ulcer; allergy; cancer; psychotic disorder; neurological disorder;
XX dyslexia; reproductive disorder; inflammatory disorder;
XX metabolic disorder.
XX
XX Unidentified.
XX
XX WO200231134-A2.
XX
XX 18-APR-2002.
XX
XX PD

PX	
PF	12-OCT-2001; 2001WO-US031874.
PR	
XX	12-OCT-2000; 2000US-0240117P.
XX	(FERR) FERRING BV.
XX	
PI	Qi S, Akinaanya XO, Riviere PJ, Junien J;
DR	WPI; 2002-444178/47.
PT	New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT	the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PS	viral infections, cancers, allergies, neurological disorders, or pain.
XX	
XX	Disclosure; Fig 3, 113pp; English.
CC	
CC	The present invention relates to the isolation of novel human serine
CC	proteases referred to as dipeptidyl peptidase IV (DPPIV)-related proteins
CC	(BPPR). The dipeptidyl peptidase IV-related proteins (DPP) and nucleic
CC	acids encoding them are useful for treating infections such as fungal,
CC	bacterial, protozoan and viral infections, particularly infections caused
CC	by human immunodeficiency virus (HIV-1 or HIV-2), pain, diabetes,
CC	precocious puberty, infertility, obesity, anorexia, bulimia, Parkinson's
CC	disease, acute heart failure, hypotension, hypertension, urinary
CC	retention, osteoporosis, angina pectoris, stroke, ulcers, asthma,
CC	allergies, cancers, migraine, vomiting, psychotic and neurological
CC	disorders (e.g. anxiety, dementia, or schizophrenia), and dyskinesias.
CC	This may also be used in discovering therapeutic agents for the
CC	treatment of reproductive, inflammatory and metabolic disorders. ABG61616
CC	-AAG61620 represent tetrapeptide amide inhibitors used to inhibit DPPIV
CC	activity
XX	
XX	
XQ	Sequence 4 AA;

```

Query Match      85.7%; Score 12; DB 5; Length 4;
Best Local Similarity 66.7%;
Matches      2; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
QY      1 TTY 3
          |||
          2 TAY 4
db

```

RESULT 7	ID	ABP67985	standard; peptide; 4 AA.
XX	AC	ABP67985;	
XX	DT	10-DEC-2002 (first entry)	
XX	DE	Human CD66 family modulating peptide SEQ ID NO 856.	
XX	KM	Human; CD66; CCR6; cytostatic; antiinflammatory; immunomodulator;	
XX	KM	antibacterial; virucide; gene therapy; vaccine; neutrophil;	
XX	KM	immune system; autoimmune disease; cancer; infection; bacterial; virus;	
XX	KM	inflammatory disease; transplantation; immunisation.	
XX	OS	Homo sapiens.	
XX	PN	WO200268601-A2.	
XX	PD	06-SEP-2002.	
XX	PF	27-FEB-2002; 2002WO-US005720.	
XX	PR	28-FEB-2001; 2001US-0272113P.	
XX	PA	(SKUBA/) SKUBITZ K M.	
XX	PA	(SKUBA/) SKUBITZ A P N.	
XX	PI	Skubitz KM, Skubitz APN;	

[illegible]

XX	RESULT 8
XX	ABP67984
ID	ABP67984 standard; peptide; 4 AA.
XX	
AC	ABP67984;
XX	
DT	10-DEC-2002 (first entry)
XX	
DE	Human CD66 family modulating peptide SEQ ID NO 855.
XX	
KW	Human, CD66, CD66CM, cytosolic; antiinflammatory; immunomodulator;
KW	antibacterial; virucide; gene therapy; vaccine; neutrophil;
KW	immune system; autoimmune disease; cancer; infection; bacterial; virus;
XX	inflammatory disease; transplantation; immunisation.
XX	
OS	Homo sapiens.
XX	
PN	WO200268601-A2.
XX	
PD	06-SEP-2002.
XX	
PF	27-FEB-2002; 2002WO-US005720.
XX	
PR	28-FEB-2001; 2001US-0272113P.
XX	
PA	(SKUB/) SKUBITZ K M.
EA	(SKUB/) SKUBITZ A P N.
XX	
P1	Skubitz KM, Skubitz APN;
XX	
DR	WPI; 2002-706981/76.
XX	
PT	New peptide from a surface exposed region of a CD66 family member, useful
PT	for modulating the function of CD66 family members, e.g. activation of
PT	neutrophils, for treating or diagnosing autoimmune diseases or cancer,
XX	and as a vaccine.
XX	

PS Claim 2; Page 47; 96pp; English.

CC The invention relates to an isolated peptide (1) from a surface exposed
CC region of a CD66 family member (ABP67130-ABP67990). The peptide
CC modulates: (a) activation of neutrophils; (b) activation or inhibition of
CC T-cells, B-cells, NK cells, LAK cells, dendritic cells or other immune
CC cells; (c) proliferation and/or differentiation of the above
CC cells, including epithelial cells; (d) homotypic and/or heterotypic
CC adhesion among CD66 family members; and (e) adhesion of CD66 family
CC members to other ligands. The peptide is useful in modulating the
CC function of CD66 family members and/or their ligands, such as activation
CC of neutrophils and activation, inhibition, proliferation and/or
CC differentiation of the immune cells. The peptides may also be used in
CC treating or diagnosing autoimmune diseases, cancer, infections (e.g.
CC bacterial or viral) or inflammatory diseases, in transplantation
CC therapies and for immunisation
XX

SQ Sequence 4 AA;

Query Match 85.7%; Score 12; DB 5; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TXY 3
| |
2 TTY 4

DB 2 TTY 4

RESULT 9
AAE38078
ID AAE38078 standard; peptide; 4 AA.

AC AAE38078;

DT 06-NOV-2003 (first entry)

DB Human 5F11 CD30 antibody VH CDR3 peptide.

XX Human; antibody; CD30; tumour; autoimmune disease; rheumatoid arthritis;
XX systemic lupus erythematosus; systemic sclerosis; Grave's disease; AICL;
XX atopic dermatitis; Hashimoto's thyroiditis; chronic renal failure; AILD;
XX acute infectious mononucleosis; angioimmunoblastic lymphadenopathy; HIV;
XX Hodgkin's disease; Castleman's disease; Kaposi's sarcoma; lymphoma; ATL;
XX adult T cell lymphoma; human immunodeficiency virus; carcinoma; therapy;
XX Wegner's granulomatosis; anaplastic large cell lymphoma; Omen's syndrome;
XX heavy chain variable domain; VH; complementarity determining region; CDR.

OS Homo sapiens.

PN WO2003059282-A2.

PD 24-JUL-2003.

PF 07-JAN-2003; 2003WO-US000440.

PR 09-JAN-2002; 2002US-0347649P.

PR 19-AUG-2002; 2002US-0404427P.

PR 06-DEC-2002; 2002US-0431684P.

PA (MEDA-) MEDAREX INC.

PI Keller T, Graziano R, Trembl J;

DR WPI; 2003-598476/56.

DR N-PSDB; AAD57390.

XX New human monoclonal antibody that binds to human CD30, useful for
XX treating or preventing tumor or autoimmune disease, e.g., rheumatoid
XX arthritis.

PS Claim 11; Page 120; 122pp; English.

CC The invention relates to human monoclonal antibody that binds to human

CC CD30. The antibody is useful for treating or preventing tumour or
CC autoimmune disease e.g. rheumatoid arthritis, systemic lupus
CC erythematosus, systemic sclerosis, atopic dermatitis, Grave's disease,
CC Hashimoto's thyroiditis, Wegner's granulomatosis, Omen's syndrome,
CC chronic renal failure, acute infectious mononucleosis, herpes or HIV
CC (human immunodeficiency virus) virus-associated diseases. The antibody is
CC also useful for treating Hodgkin's disease, anaplastic large cell
CC lymphoma (ALCL), adult T cell lymphoma (ATL), angioimmunoblastic
CC lymphadenopathy (AILD)-like T cell lymphoma, HIV associated body cavity
CC based lymphomas, embryonal carcinomas, undifferentiated carcinomas of the
CC rhino-pharynx (e.g. Schminke's tumour), Castleman's disease, Kaposi's
CC Sarcoma and other T-cell or B-cell lymphomas. The present sequence is
CC human CD30 antibody VH (heavy chain variable domain) CDR (complementarity
CC determining region) peptide
XX

SQ Sequence 4 AA;

Query Match 85.7%; Score 12; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TXY 3
| |
2 TTY 4

DB 2 TTY 4

RESULT 10

ADCC4564
ID ADCC4564 standard; peptide; 4 AA.

AC ADCC4564;

DT 01-JAN-2004 (first entry)

DB Mutant phage sequence #10.

XX anti-CD22 antibody; RFB4; Cytostatic; Gene therapy; CD22-Antagonist;
XX cancer; phage; mutant; mutein.

OS Unidentified.

PN WO2003027135-A2.

PD 03-APR-2003.

PF 25-SEP-2002; 2002WO-US030316.

PR 26-SEP-2001; 2001US-0325360P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Pastan IH, Salvatore G, Beers R, Kreltman RJ;

DR WPI; 2003-402972/38.

XX New anti-CD22 antibody, useful for the manufacture of a medicament for
XX detecting or inhibiting growth of CD22+ cancer cell, comprising variable
XX heavy and light chains of RFB4 antibody.

PS Example 1; SEQ ID NO 22; 59pp; English.

CC The present invention relates to a new anti-CD22 antibody has variable
CC light (VL) and variable heavy (VH) chains of the antibody RFB4. The anti-
CC CD22 antibody is useful for the manufacture of a medicament for detecting
CC or inhibiting growth of CD22+ cancer cell. The present sequence
CC represents a mutant phage sequence of the invention.

SQ Sequence 4 AA;

Query Match 85.7%; Score 12; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TXY 3
DB 2 TAY 4

RESULT 11
AAP71550
ID AAP71550 standard; protein; 5 AA.

XX AAP71550;

DT 25-MAR-2003 (revised)
07-MAY-1991 (first entry)

DE AIDS virus receptor site blocking peptide (III).

KW AIDS; virus; receptor site; HIV; vaccine; antibodies.

OS Synthetic.

PN BP249390-A.

PD 16-DEC-1987.

PF 03-JUN-1987; 87EP-00304913.

PR 03-JUN-1986; 86US-00869919.

PR 26-JUN-1986; 86US-00878586.

PR 12-DEC-1986; 86US-00940919.

PR 11-MAY-1987; 87US-00048148.

PR 03-JUN-1987; 87EP-00304939.

XX (PERT/) PERT C B.

PA (USDC) US SEC OF COMMERCE.

PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

PA (USGO) US GOVERNMENT.

PI Pert CB, Ruff MR, Farrar WL;

DR WPI; 1987-350068/50.

PT New peptide(s) related to AIDS virus - which inhibit AIDS virus binding

PT to receptor sites and prevent cell infectivity with AIDS virus.

XX Claim 5; Page 9; 12pp; English.

XX This peptide is a specifically claimed example of a highly generic

CC formula. The peptide blocks effectively receptor sites of cells and

CC prevents cell infectivity with AIDS virus in monkey, rat and human brain

CC membranes and cells of the immune system. Vaccine preps. contg. the

CC peptide provide protection against infection by AIDS virus. The peptide

CC can also be used in kits for the detection of the AIDS virus and

CC antibodies to the AIDS virus; and as immunogens to elicit monoclonal

CC antibodies. The peptide may be produced by conventional methods of

CC peptide synthesis using solid phase or liquid phase methods. See also

CC AAP71548-56, and EP-249394. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 5 AA;

Query Match 85.7%; Score 12; DB 1; Length 5;

Best Local Similarity 66.7%; Pred. No. 1.7e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TXY 3

DB 2 TSY 4

RESULT 12

AAP71551

XX AAP71551 standard; protein; 5 AA.

XX 25-MAR-2003 (revised)
DT 07-MAY-1991 (first entry)

DE AIDS virus receptor site blocking peptide (IV).

KW AIDS; virus; receptor site; HIV; vaccine; antibodies.

OS Synthetic.

PN BP249390-A.

PD 16-DEC-1987.

PF 03-JUN-1987; 87EP-00304913.

PR 03-JUN-1986; 86US-00869919.

PR 26-JUN-1986; 86US-00878586.

PR 12-DEC-1986; 86US-00940919.

PR 11-MAY-1987; 87US-00048148.

PR 03-JUN-1987; 87EP-00304939.

XX (PERT/) PERT C B.

PA (USDC) US SEC OF COMMERCE.

PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

PA (USGO) US GOVERNMENT.

PI Pert CB, Ruff MR, Farrar WL;

DR WPI; 1987-350068/50.

PT New peptide(s) related to AIDS virus - which inhibit AIDS virus binding

PT to receptor sites and prevent cell infectivity with AIDS virus.

XX Claim 5; Page 9; 12pp; English.

XX This peptide is a specifically claimed example of a highly generic

CC formula. The peptide blocks effectively receptor sites of cells and

CC prevents cell infectivity with AIDS virus in monkey, rat and human brain

CC membranes and cells of the immune system. Vaccine preps. contg. the

CC peptide provide protection against infection by AIDS virus. The peptide

CC can also be used in kits for the detection of the AIDS virus and

CC antibodies to the AIDS virus; and as immunogens to elicit monoclonal

CC antibodies. The peptide may be produced by conventional methods of

CC peptide synthesis using solid phase or liquid phase methods. See also

CC AAP71548-56, and EP-249394. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 5 AA;

Query Match 85.7%; Score 12; DB 1; Length 5;

Best Local Similarity 66.7%; Pred. No. 1.7e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TXY 3

DB 2 TSY 4

RESULT 13

AAP71555

XX AAP71555 standard; protein; 5 AA.

XX AAP71555;

DT 25-MAR-2003 (revised)

DT 07-MAY-1991 (first entry)

DE AIDS virus receptor site blocking peptide (VIII).

KW AIDS; virus; T4 receptor site; HIV; vaccine; antibodies.

OS Synthetic.

```

PR      03 -JUN-1987;      87EP-00304939.
XX
XX      (PERT/)  PERT C B.
PA      (USDC)   US SEC OF COMMERCE.
PA      (USSH)   US DEPT HEALTH & HUMAN SERVICE.
PA      (USGO)   US GOVERNMENT.
XX
XX      Pert CB, Ruff MR, Farrar WL;
PI
XX      WPI; 1987-350068/50.
XX
XX      New peptide(s) related to AIDS virus - which inhibit AIDS virus binding
PT      to receptor sites and prevent cell infectivity with AIDS virus.
XX
XX      Claim 5; Page 9; 12pp; English.
XX
XX      This peptide is a specifically claimed example of a highly generic
CC      formula. The peptide blocks effectively receptor sites of cells and
CC      prevents cell infectivity with AIDS virus in monkey, rat and human brain
CC      membranes and cells of the immune system. Vaccine preps. contg. the
CC      peptide provide protection against infection by AIDS virus. The peptide
CC      can also be used in kits for the detection of the AIDS virus and
CC      antibodies to the AIDS virus; and as immunogens to elicit monoclonal
CC      antibodies. The peptide may be produced by conventional methods of
CC      peptide synthesis using solid phase or liquid phase methods. See also
XX      AAP71548-56, and EP-249394. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX      Sequence 5 AA;
SQ
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XX      Query Match      85.7%; Score 12; DB 1; Length 5;
XX      Best Local Similarity 66.7%; Pred. No. 1.7e+06;
XX      Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      QY      1 TXY 3
XX      |
XX      |
XX      Db      2 TSY 4

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Query Match	85.7%;	Score 12;	DB 1;	Length 5;
Best Local Similarity	66.7%;	Pred. No. 1.7e+06;		
Matches	2;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0

QY	1	TXV	3	
Db	2	TSY	4	

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RESULT 14
AAP71552
ID AAP71552 standard; protein; 5 AA.
vv

```

DT	25-MAR-2003	(revised)
DT	07-MAY-1991	(first entry)
XY		

DE
xx

AIDS virus receptor site blocking peptide (V).

KM AIDS; virus; receptor site; HIV; vaccine; antibodies.
 XX

OS Synthetic.

PN EP249390-A.
vv

PD 16-DEC-1987

PF 03-JUN-1987; 87EP-00304913.

PR 03-JUN-1986; 86US-00869919.

PR 12-DEC-1986; 86US-00940919.

1000

```

RESULT 15
AAP83009
ID AAP83009 standard; protein; 5 AA
XX

```

DT	25-MAR-2003	(revised)
DT	10-DEC-1990	(first entry)

Blocking peptide used in composition for treatment and diagnosis of HIV

HIV; gp110; monoclonal antibodies; neutralising region

OS Homo sapiens.

PN GB2196634-A.

PD 05-MAY-1988

PE 19-AUG-1987;

PR 20-AUG-1986

PR 29-JUN-1987

XX

XX

[illegible][illegible]

PT of human imm

Monoclonal antibodies and peptide(s) - useful for treatment and diagnosis of human immunodeficiency virus infections.

XX Claim 42; Page 24; 25pp; English.
PS
XX
CC This is a blocking peptide which inhibits virus proliferation. It is
CC useful, in conjunction with a monoclonal antibody to a neutralizing
CC region of HIV, for treatment or prophylaxis of HIV infections. N- and C-
CC terminals can have up to 20 amino acids attached. See also AAPP3003-08
CC and AAPP3010-12. This is equivalent to N18701950 (accession no. is from
CC this). (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-
CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct DR field.)
XX
SQ Sequence 5 AA;
Query Match 85.7%; Score 12; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TXY 3
| |
| |
Db 2 TSY 4

Search completed: December 13, 2004, 22:22:42
Job time : 82 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:12:37 ; Search time 21.4 Seconds
(without alignments)
12.396 Million cell updates/sec

Title: US-10-068-905-9

Perfect score: 14

Sequence: 1 TXVX 4

Scoring table: BLOSUM62

Searched: Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	85.7	4	1 US-08-302-829-9	Sequence 9, Appl
2	12	85.7	4	3 US-09-082-837A-9	Sequence 9, Appl
3	12	85.7	4	3 US-09-421-845-9	Sequence 9, Appl
4	12	85.7	5	1 US-08-385-443-5	Sequence 9, Appl
5	12	85.7	5	1 US-08-302-829-8	Sequence 8, Appl
6	12	85.7	5	1 US-08-481-840A-6	Sequence 8, Appl
7	12	85.7	5	1 US-08-403-718-8	Sequence 8, Appl
8	12	85.7	5	1 US-08-619-462-8	Sequence 8, Appl
9	12	85.7	5	3 US-09-082-837A-8	Sequence 8, Appl
10	12	85.7	5	3 US-08-331-625A-14	Sequence 8, Appl
11	12	85.7	5	3 US-09-421-845-8	Sequence 14, Appl
12	12	85.7	5	3 US-09-494-151-14	Sequence 14, Appl
13	12	85.7	5	4 US-09-972-484-14	Sequence 15, Appl
14	12	85.7	5	4 US-09-628-665-15	Sequence 15, Appl
15	12	85.7	5	5 5276016-4	Patent No. 5276016
16	12	85.7	5	5 5276016-8	Patent No. 5276016
17	12	85.7	5	5 5276016-10	Patent No. 5276016
18	12	85.7	5	5 5276016-11	Patent No. 5276016
19	12	85.7	5	5 5276016-13	Patent No. 5276016
20	12	85.7	5	5 5276016-18	Patent No. 5276016
21	12	85.7	6	3 US-08-392-459-40	Sequence 15, Appl
22	12	85.7	6	3 US-09-428-302-15	Sequence 15, Appl
23	12	85.7	6	4 US-09-854-799-40	Sequence 40, Appl
24	12	85.7	6	4 PCT-US91-08525-40	Sequence 40, Appl
25	12	85.7	7	2 US-08-739-401A-6	Sequence 6, Appl
26	12	85.7	7	3 US-09-443-501A-20	Sequence 20, Appl
27	12	85.7	7	3 US-08-672-213-33	Sequence 33, Appl

28	12	85.7	7	4 US-09-622-166A-21	Sequence 21, Appl
29	12	85.7	7	4 US-09-282-029A-121	Sequence 121, App
30	12	85.7	7	4 US-09-185-908-121	Sequence 121, App
31	12	85.7	7	6 5169935-6	Patent No. 5169935
32	12	85.7	8	1 US-08-159-340A-26	Sequence 26, Appl
33	12	85.7	8	1 US-08-302-829-11	Sequence 35, Appl
34	12	85.7	8	1 US-08-389-459A-15	Sequence 11, Appl
35	12	85.7	8	2 US-08-922-267A-64	Sequence 15, Appl
36	12	85.7	8	3 US-09-082-837A-11	Sequence 64, Appl
37	12	85.7	8	3 US-08-159-339A-1162	Sequence 11, Appl
38	12	85.7	8	3 US-08-444-818-400	Sequence 1045, Ap
39	12	85.7	8	3 US-08-987-867A-15	Sequence 15, Appl
40	12	85.7	8	3 US-08-421-845-11	Sequence 400, App
41	12	85.7	8	3 US-08-845-541B-25	Sequence 11, Appl
42	12	85.7	8	3 US-08-845-541B-26	Sequence 25, Appl
43	12	85.7	8	3 US-08-845-541B-26	Sequence 26, Appl
44	12	85.7	8	3 US-08-845-541B-26	Sequence 28, Appl
45	12	85.7	8	3 US-08-845-541B-26	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-302-829-9
; Sequence 9, Application US/08302829
; Patent No. 5756449
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Anders J
; APPLICANT: ASTON, Roger
; APPLICANT: CARLEN, Peter L
; APPLICANT: DOOB, Penelope R
; APPLICANT: MACFADDEN, Douglas K
; APPLICANT: PHIPPS, David J
; APPLICANT: RATHEN, Deborah
; APPLICANT: WIDMER, Fred
; TITLE OF INVENTION: Peptide T and Related Peptides in the
; TITLE OF INVENTION: Treatment of Inflammation, Including Multiple Sclerosis
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,829
; FILING DATE: 29-MAR-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00649
; FILING DATE: 29-MAR-1993
; APPLICATION NUMBER: US 07/987,674
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/915,118
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 645/92
; FILING DATE: 14-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/858,832
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McDermott, John J
; REGISTRATION NUMBER: 26949

REFERENCE/DOCKET NUMBER: 94,772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..4
OTHER INFORMATION: /note="aal is D-Thr, aa4 is D-Thr"
US-08-302-829-9

Query Match 85.7%; Score 12; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
DB 1 TTY 3

RESULT 2
US-09-082-837A-9
Sequence 9, Application US/09082837A
Patent No. 6011014
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Anders J
APPLICANT: ASTON, Roger
APPLICANT: CARLEN, Peter L
APPLICANT: DOOB, Penelope R
APPLICANT: MACFADDEN, Douglas K
APPLICANT: PHIPPS, David J
APPLICANT: RATHJEN, Deborah
APPLICANT: WIDMER, Fred
TITLE OF INVENTION: Peptide T and Related Peptides in the Treatment of
TITLE OF INVENTION: Inflammation, Including Multiple Sclerosis
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 10 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,837A
FILING DATE: 21-JUN-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,829
FILING DATE: 29-MAR-1993
PRIOR APPLICATION DATA: NO PCT/GB93/00649
APPLICATION NUMBER: 29-MAR-1993
FILING DATE: 29-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,674
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/915,118
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA: DK 645/92
APPLICATION NUMBER: 14-MAY-1992
FILING DATE: 14-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,832
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dreikoff, W. Dennis
REGISTRATION NUMBER: 27193
REFERENCE/DOCKET NUMBER: 94,772-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..4
OTHER INFORMATION: /note="aal is D-Thr, aa4 is D-Thr"
US-09-082-837A-9

Query Match 85.7%; Score 12; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
DB 1 TTY 3

RESULT 3
US-09-421-845-9
Sequence 9, Application US/09421845
Patent No. 625374
GENERAL INFORMATION:
APPLICANT: Jorgensen
APPLICANT: Aston
APPLICANT: Carlen
APPLICANT: Doob
APPLICANT: MacFadden
APPLICANT: Phipps
APPLICANT: Rathjen
APPLICANT: Widmer
TITLE OF INVENTION: Peptide T and Related Peptides in the Treatment of
TITLE OF INVENTION: Inflammation, Including Multiple Sclerosis
FILE REFERENCE: Peptide T Inflammation
CURRENT APPLICATION NUMBER: US/09/421,845
CURRENT FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: 09/082,837
PRIOR FILING DATE: 1998-05-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(4)
OTHER INFORMATION: Thr at positions 1 and 4 are both D-Thr.
US-09-421-845-9

Query Match 85.7%; Score 12; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
DB 1 TTY 3

RESULT 4
US-08-385-443-5
Sequence 5, Application US/08385443
Patent No. 5534495
GENERAL INFORMATION:
APPLICANT: PERT, CANDANCE B.
APPLICANT: RUFF, MICHAEL R.
TITLE OF INVENTION: TREATMENT OF NON-HIV NEUROPATHIC
TITLE OF INVENTION: PAIN SYNDROMES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: JULES E. GOLDBERG
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,443
FILING DATE: 08-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/067,523
FILING DATE: 23-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
REFERENCE/DOCKET NUMBER: ADVANCED PEPTIDES P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-385-443-5

Query Match 85.7%; Score 12; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 TXY 3
1 1 1
2 TSY 4

Db

RESULT 5
US-08-302-829-8
Sequence 8, Application US/08302829
Patent No. 5756449
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Anders J
APPLICANT: ASTON, Roger
APPLICANT: CARLEN, Peter L.
APPLICANT: DOOB, Penelope R.
APPLICANT: MACFADDEN, Douglas K
APPLICANT: PHILIPS, David J
APPLICANT: RATHEN, Deborah
APPLICANT: WIDMER, Fred
TITLE OF INVENTION: Peptide T and Related Peptides in the
TITLE OF INVENTION: Treatment of Inflammation, Including Multiple Sclerosis
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & ALLEGRETTI, LTD.
STREET: 10 S. Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,829
FILING DATE: 29-MAR-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00649
FILING DATE: 29-MAR-1993
APPLICATION NUMBER: US 07/987,674
FILING DATE: 09-DEC-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/915,118
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 645/92
FILING DATE: 14-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,832
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: McDONNELL, John J
REGISTRATION NUMBER: 26949
REFERENCE/DOCKET NUMBER: 94,772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-302-829-8

Query Match 85.7%; Score 12; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 TXY 3
1 1 1
2 TSY 4

Db

RESULT 6
US-08-481-840A-6
Sequence 6, Application US/08481840A
Patent No. 5763406
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Ove
APPLICANT: MACFADDEN, D.
TITLE OF INVENTION: Peptides for Treatment
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,840A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,777
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Iwanicki, John P
REGISTRATION NUMBER: 34,628
REFERENCE/DOCKET NUMBER: 93,741-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-840A-6

Query Match 85.7%; Score 12; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRY 3
DB 2 TSY 4

RESULT 7
US-08-403-718-8
Sequence 8, Application US/08403718
Patent No. 5795858
GENERAL INFORMATION:
APPLICANT: MICHAELIS, JURGEN
APPLICANT: SLEIGH, MERILYN J.
TITLE OF INVENTION: TREATMENT OR PREVENTION OF CROHN'S
DISEASE AND/OR ULCERATIVE COLITIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,718
FILING DATE: 31-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-74
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (704) 816-4100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-403-718-8

Query Match 85.7%; Score 12; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRY 3
DB 2 TSY 4

RESULT 8
US-08-619-462-8
Sequence 8, Application US/08619462
Patent No. 5798335
GENERAL INFORMATION:
APPLICANT: MICHAELIS, JURGEN
APPLICANT: TRIGG, Timothy Elliot
TITLE OF INVENTION: METHOD FOR THE TREATMENT OR PREVENTION OF
ECZEMA/DERMATITIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,462
FILING DATE: 07-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-84
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (704) 816-4100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-619-462-8

Query Match 85.7%; Score 12; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRY 3
DB 2 TSY 4

RESULT 9
US-09-082-837A-8
Sequence 8, Application US/09082837A
Patent No. 6011014
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Anders J
APPLICANT: ASTON, Roger
APPLICANT: CARLEN, Peter L
APPLICANT: DOOB, Penelope R
APPLICANT: MACFADDEN, Douglas K
APPLICANT: PHIPPS, David J

APPLICANT: RATHJEN, Deborah
APPLICANT: WIDMER, Fred
TITLE OF INVENTION: Peptide T and Related Peptides in the Treatment of
TITLE OF INVENTION: Inflammation, Including Multiple Sclerosis
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 10 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,837A
FILING DATE: 21-JUN-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,829
FILING DATE: 29-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00649
FILING DATE: 29-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,674
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/915,118
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 645/92
FILING DATE: 14-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,832
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Drehkoff, W. Dennis
REGISTRATION NUMBER: 27193
REFERENCE/DOCKET NUMBER: 94,772-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: peptide
US-09-082-837A-8

Query Match 85.7%; Score 12; DB 3; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
Db 2 TSY 4

RESULT 10
US-08-331-625A-14
Sequence 14, Application US/08331625A
Patent No. 6057436
GENERAL INFORMATION:
APPLICANT: Miller, Timothy J.
APPLICANT: Kieffer, Sharon
APPLICANT: Reed, Albert Paul
APPLICANT: Jones, Elaine V.

TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation - Corporate
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,625A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/880,194
FILING DATE: 08-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-331-625A-14

Query Match 85.7%; Score 12; DB 3; Length 5;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
Db 3 TAY 5

RESULT 11
US-09-421-845-8
Sequence 8, Application US/09421845
Patent No. 6265374
GENERAL INFORMATION:
APPLICANT: Jorgensen
APPLICANT: Astor
APPLICANT: Carlen
APPLICANT: Doob
APPLICANT: Macfadden
APPLICANT: Phipps
APPLICANT: Rathjen
APPLICANT: Widmer
TITLE OF INVENTION: Inflammation, Including Multiple Sclerosis.
FILE REFERENCE: Peptide T Inflammation
CURRENT APPLICATION NUMBER: US/09/421,845
FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: 09/082,837
PRIOR FILING DATE: 1998-05-21

Peptide T and Related Peptides in the Treatment of

NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 8
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-09-421-845-8

Query Match
Best Local Similarity 85.7%; Score 12; DB 3; Length 5;
Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
| |
Db 2 TXY 4

RESULT 12
US-09-494-151-14
Sequence 14, Application US/09494151
Patent No. 6372224
GENERAL INFORMATION:

APPLICANT: Miller, Timothy J.
Klepfier, Sharon
Reed, Albert Paul
Jones, Elaine V.

TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
Therefor

NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation - Corporate
Patents

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA

COUNTRY: USA
ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/331,625
FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991

APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990

ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.

REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015

TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids

TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-494-151-14

Query Match
Best Local Similarity 85.7%; Score 12; DB 3; Length 5;
Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
| |
Db 3 TXY 5

RESULT 13
US-09-972-484-14
Sequence 14, Application US/09972484
Patent No. 6602504
GENERAL INFORMATION:

APPLICANT: Miller, Timothy J.
Klepfier, Sharon
Reed, Albert Paul
Jones, Elaine V.

TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
Therefor

NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation - Corporate
Patents

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA

COUNTRY: USA
ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/972,484
FILING DATE: 05-Oct-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000

APPLICATION NUMBER: 08/331,625
FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991

APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990

ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.

REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015

TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids

TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-972-484-14

Query Match
Best Local Similarity 85.7%; Score 12; DB 4; Length 5;
Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
| |
Db 3 TXY 5

RESULT 14
US-09-628-665-15
Sequence 15, Application US/09628665
Patent No. 6673771
GENERAL INFORMATION:

APPLICANT: Greene, Mark I.
APPLICANT: Murali, Ramachandran
APPLICANT: Kinoshaki, Masahiko
TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
FILE REFERENCE: UPN3831
CURRENT APPLICATION NUMBER: US/09/628,665
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146,094
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 15
LENGTH: 5
TYPE: prt
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6673771e1 Sequence
US-09-628-665-15

Query Match 85.7% Score 12; DB 4; Length 5;
Best Local Similarity 66.7% Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TXY 3
| |
| |
Db 1 TSY 3

RESULT 15
5276016-4
Patent No. 5276016
APPLICANT: PERT, CANDACE B.; RUFF, WILLIAM R.
FARRAR, WILLIAM L.
TITLE OF INVENTION: SMALL PEPTIDES WHICH INHIBIT
BINDING TO T-4 RECEPTORS AND ACT AS IMMUNOGENS
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/568,616
FILING DATE: 16-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 314,507
FILING DATE: 15-FEB-1989
APPLICATION NUMBER: 48,148
FILING DATE: 11-MAY-1987
APPLICATION NUMBER: 878,586
FILING DATE: 26-JUN-1986
APPLICATION NUMBER: 869,919
FILING DATE: 03-JUN-1986
SEQ ID NO: 4
LENGTH: 5
5276016-4

Query Match 85.7% Score 12; DB 6; Length 5;
Best Local Similarity 66.7% Pred. No. 3.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TXY 3
| |
| |
Db 2 TSY 4

Search Completed: December 13, 2004, 22:34:52
Job time : 22.4 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:31:47 ; Search time 68.6 Seconds
(without alignments)
20.927 Million cell updates/sec

Title: US-10-068-905-9

Perfect score: 14

Sequence: 1 TXXX 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/pubppaa/PC7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	85.7	4	US-10-285-045-53	Sequence 53, Appl
2	12	85.7	4	US-10-284-660-53	Sequence 53, Appl
3	12	85.7	4	US-10-338-366-42	Sequence 42, Appl
4	12	85.7	5	US-09-972-484-14	Sequence 14, Appl
5	12	85.7	5	US-10-181-937-57	Sequence 57, Appl
6	12	85.7	6	US-09-854-799-40	Sequence 40, Appl
7	12	85.7	6	US-09-727-963-82	Sequence 82, Appl
8	12	85.7	6	US-10-272-411-26	Sequence 26, Appl
9	12	85.7	6	US-10-272-328A-26	Sequence 26, Appl
10	12	85.7	6	US-10-285-045-61	Sequence 61, Appl
11	12	85.7	6	US-10-284-660-61	Sequence 61, Appl
12	12	85.7	6	US-10-304-059-42	Sequence 42, Appl
13	12	85.7	6	US-10-284-569-7	Sequence 7, Appl

14	12	85.7	6	15	US-10-646-874-40	Sequence 40, Appl
15	12	85.7	7	8	US-08-701-278-14	Sequence 14, Appl
16	12	85.7	7	9	US-09-727-889-20	Sequence 20, Appl
17	12	85.7	7	9	US-09-996-288-81	Sequence 81, Appl
18	12	85.7	7	9	US-09-996-288-85	Sequence 85, Appl
19	12	85.7	7	9	US-09-996-288-143	Sequence 143, Appl
20	12	85.7	7	9	US-09-996-288-145	Sequence 145, Appl
21	12	85.7	7	9	US-09-996-288-147	Sequence 147, Appl
22	12	85.7	7	9	US-09-996-288-149	Sequence 149, Appl
23	12	85.7	7	9	US-09-185-908-121	Sequence 121, Appl
24	12	85.7	7	10	US-09-992-886-29	Sequence 29, Appl
25	12	85.7	7	10	US-09-996-285-81	Sequence 81, Appl
26	12	85.7	7	10	US-09-996-285-85	Sequence 85, Appl
27	12	85.7	7	10	US-09-996-285-143	Sequence 143, Appl
28	12	85.7	7	10	US-09-996-285-145	Sequence 145, Appl
29	12	85.7	7	10	US-09-996-285-147	Sequence 147, Appl
30	12	85.7	7	10	US-09-996-285-149	Sequence 149, Appl
31	12	85.7	7	10	US-09-954-385-41	Sequence 41, Appl
32	12	85.7	7	14	US-10-162-004-7	Sequence 7, Appl
33	12	85.7	7	14	US-10-162-004-8	Sequence 8, Appl
34	12	85.7	7	14	US-10-162-004-9	Sequence 9, Appl
35	12	85.7	7	14	US-10-052-578-224	Sequence 224, Appl
36	12	85.7	7	14	US-10-190-082-653	Sequence 653, Appl
37	12	85.7	7	14	US-10-304-059-8	Sequence 8, Appl
38	12	85.7	7	14	US-10-160-506-103	Sequence 103, Appl
39	12	85.7	7	14	US-10-286-457-115	Sequence 115, Appl
40	12	85.7	7	14	US-10-022-066-234	Sequence 234, Appl
41	12	85.7	7	14	US-10-053-520-224	Sequence 224, Appl
42	12	85.7	7	14	US-10-423-007-21	Sequence 21, Appl
43	12	85.7	7	14	US-10-053-498B-224	Sequence 224, Appl
44	12	85.7	7	14	US-10-237-405-17	Sequence 17, Appl
45	12	85.7	7	15	US-10-461-863-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-10-285-045-53
; Sequence 53, Application US/10285045
; Publication No. US20030147904A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahn Seong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Salzman
; TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED
; FILE REFERENCE: 51158-20011.10
; CURRENT APPLICATION NUMBER: US/10/285,045
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/547,789
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/128,858
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-285-045-53

Query Match
Best Local Similarity 85.7%; Score 12; DB 14; Length 4;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TXY 3
1 1
1 TTY 3
Db

RESULT 2

US-10-284-660-53
; Sequence 53, Application US/10284660
; Publication No. US20030157521A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED
; FILE REFERENCE: 5158-2001.01
; CURRENT APPLICATION NUMBER: US/10/284,660
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: US 09/547,789
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/128,858
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-284-660-53

Query Match

Best Local Similarity 85.7%; Score 12; DB 14; Length 4;
Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
|
|
|
Db 1 TTY 3

RESULT 3

US-10-338-366-42
; Sequence 42, Application US/10338366
; Publication No. US20040006215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Graziano, Robert
; APPLICANT: Trembl, John
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
; FILE REFERENCE: MX1-180
; CURRENT APPLICATION NUMBER: US/10/338,366
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/347649
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/404427
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/431684
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-366-42

Query Match 85.7%; Score 12; DB 15; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
|
|
|
Db 2 TAY 4

RESULT 4
US-09-972-484-14

; Sequence 14, Application US/09972484
; Patent No. US20020127245A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; THEREFOR

NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation - Corporate
Patents
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,484
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/494,151
FILING DATE: 28-Jan-2000
APPLICATION NUMBER: 08/331,625
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990

ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC H85010-1
TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-972-484-14

Query Match 85.7%; Score 12; DB 9; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
|
|
|
Db 3 TAY 5

RESULT 5
US-10-181-937-57
; Sequence 57, Application US/10181937
; Publication No. US20040055022A1
; GENERAL INFORMATION:
; APPLICANT: Cheng, Nick
; APPLICANT: Gagnier, Liane
; APPLICANT: Ueffler, Wilfred A.
; TITLE OF INVENTION: Compositions and Methods for Screening Therapeutic
; FILE REFERENCE: 020739-000410US

CURRENT APPLICATION NUMBER: US/10/181,937
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/181,091
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: WO PCT/CA01/00133
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 57
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: mp97 and hp97
US-10-181-937-57

Query Match 85.7%; Score 12; DB 15; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
3 TTY 5

Db

RESULT 6
US-09-854-799-40
Sequence 40, Application US/09854799
Patent No. US20020115064A1
GENERAL INFORMATION:

APPLICANT: SmithKline Beecham, Corporation
TITLE OF INVENTION: Recombinant Feline Coronavirus S
Proteins

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESS: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-2799

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,799

FILING DATE: 14-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/392,459

FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/613,066

FILING DATE: 14-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: King, William T.

REGISTRATION NUMBER: 30,954

REFERENCE/DOCKET NUMBER: SEC 14532B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 270-5015

TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-854-799-40

Query Match 85.7%; Score 12; DB 9; Length 6;

Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
4 TAY 6

Db

RESULT 7
US-09-727-963A-82

Sequence 82, Application US/09727963A

Patent No. US2002015106A1

GENERAL INFORMATION:

APPLICANT: V.I. Technologies, Inc.

APPLICANT: Hammond, David J.

TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE

FILE REFERENCE: 18242-505

CURRENT APPLICATION NUMBER: US/09/727,963A

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557

PRIOR FILING DATE: 1999-12-02

NUMBER OF SEQ ID NOS: 99

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 82

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand

NAME/KEY: VARIANT

LOCATION: (1)

OTHER INFORMATION: wherein Xaa is D-phenylalanine

US-09-727-963A-82

Query Match 85.7%; Score 12; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
4 TSY 6

Db

RESULT 8
US-10-272-411-26

Sequence 26, Application US/10272411

Publication No. US20030100068A1

GENERAL INFORMATION:

APPLICANT: Barnes Jewish Hospital

APPLICANT: Lam, Jonathan

APPLICANT: Rose, F. Patrick

APPLICANT: Reitelbaum, Steven

TITLE OF INVENTION: RANKL KINICS AND USES THEREOF

FILE REFERENCE: 60019620-0202

CURRENT APPLICATION NUMBER: US/10/272,411

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 60/329,393

PRIOR FILING DATE: 2001-10-15

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patent In version 3.1

SEQ ID NO 26

LENGTH: 6

TYPE: PRT

ORGANISM: Homo sapiens

US-10-272-411-26

Query Match 85.7%; Score 12; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
1 TSY 3

Db

RESULT 9
US-10-272-328A-26
; Sequence 26, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, P. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-328A-26

Query Match 85.7%; Score 12; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
Db 4 TTY 6

RESULT 10
US-10-285-045-61
; Sequence 61, Application US/10285045
; Publication No. US20030147904A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED
; TITLE OF INVENTION: IN PROSTATE CANCER
; FILE REFERENCE: 51158-2001.10
; CURRENT APPLICATION NUMBER: US/10/285,045
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/547,789
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/128,858
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-285-045-61

Query Match 85.7%; Score 12; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
Db 4 TTY 6

RESULT 11
US-10-284-660-61
; Sequence 61, Application US/10284660

; Publication No. US20030157521A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED
; TITLE OF INVENTION: IN PROSTATE CANCER
; FILE REFERENCE: 51158-2001.01
; CURRENT APPLICATION NUMBER: US/10/284,660
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: US 09/547,789
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/128,858
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-284-660-61

Query Match 85.7%; Score 12; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
Db 4 TTY 6

RESULT 12
US-10-304-059-42
; Sequence 42, Application US/10304059
; Publication No. US20030158141A1
; GENERAL INFORMATION:
; APPLICANT: GROMETTER, Mathias
; APPLICANT: DOBRIKOVA, Elena Y
; TITLE OF INVENTION: GENETICALLY STABLE EXPRESSION VECTOR
; FILE REFERENCE: 1579-769
; CURRENT APPLICATION NUMBER: US/10/304,059
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/332,554
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Poliovirus
US-10-304-059-42

Query Match 85.7%; Score 12; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
Db 3 TTY 5

RESULT 13
US-10-284-569-7
; Sequence 7, Application US/10284569
; Publication No. US20030220266A1
; GENERAL INFORMATION:
; APPLICANT: Jabbour, Henry Nicolas
; APPLICANT: Sales, Kurt Jason
; APPLICANT: Katz, Arleh

Query Match	Score 12;	DB 15;	Length 6
Best Local Similarity	85.7%;	Pred. No. 1.4e+06;	
	66.7%;		

Search completed: December 13, 2004, 23:02:41
Job time : 69.6 secs

Search completed: December 13, 2004, 23:02:41
Job time : 69.6 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:01:21 ; Search time 15.2 Seconds
(Without alignments)
25.320 Million cell updates/sec

Title: US-10-068-905-9
Perfect score: 14
Sequence: 1 TXYX 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.79.*
2: PIR1.*
3: PIR2.*
4: PIR3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	85.7	12	2 PA0037	plascocyanin 2 - A
2	12	85.7	13	2 PC1149	equinotoxin 1A - s
3	12	85.7	14	2 B39111	ig heavy chain V r
4	12	85.7	17	2 PH1630	ig H chain V-D-J r
5	12	85.7	18	2 A43826	dnak-type molecula
6	12	85.7	18	2 S70612	alpha-microglobuli
7	12	85.7	18	2 PL0025	T-cell surface gly
8	12	85.7	20	2 PH1783	T-cell receptor al
9	12	85.7	20	2 I65242	homeotic protein H
10	12	85.7	22	2 IS1291	fam6 protein - Esc
11	12	85.7	23	2 B42382	replication initia
12	12	85.7	24	2 PH1713	ig heavy chain V r
13	12	85.7	24	2 PH1712	ig heavy chain V r
14	12	85.7	24	2 B27262	nicotinic acetylch
15	12	85.7	25	2 JH0701	omega-conotoxin MV
16	12	85.7	25	2 PH1716	ig heavy chain V r
17	12	85.7	25	2 IS1151	alpha actin - qua
18	12	85.7	25	2 JAO171	dnak-type molecula
19	12	85.7	25	2 A47424	nontoxic type 2 ri
20	12	85.7	26	2 C44379	omega-conotoxin SV
21	12	85.7	26	2 F37396	pollen allergen Ag
22	12	85.7	26	2 F37396	pollen allergen Ag
23	12	85.7	26	2 G37396	pollen allergen Ag
24	12	85.7	27	2 B32112	R15 beta peptide -
25	12	85.7	27	2 A84502	probable C-1-tetra
26	12	85.7	27	2 I57683	parathyroid hormon
27	12	85.7	28	2 I32529	ig lambda chain V
28	12	85.7	28	2 I45911	dnak-type molecula
29	12	85.7	29	1 A55527	pyrroloquinoline q

30	12	85.7	29	2 B81006	hypothetical prote
31	12	85.7	30	2 PH0249	T-cell receptor Vb
32	12	85.7	30	2 S66448	trimethylamine deh
33	12	85.7	30	2 S23365	T-cell receptor al
34	12	85.7	30	2 D82251	hypothetical prote
35	12	85.7	31	1 D64117	fish protein homol
36	12	85.7	31	2 C95215	hypothetical prote
37	12	85.7	31	2 H66822	hypothetical prote
38	12	85.7	31	2 S05124	hypothetical prote
39	12	85.7	31	2 S58569	hypothetical prote
40	12	85.7	31	2 T09121	hypothetical prote
41	12	85.7	31	2 T14568	hypothetical prote
42	12	85.7	32	2 S57230	hypothetical prote
43	12	85.7	32	2 S57233	sex combs reduced
44	12	85.7	33	2 S22605	ribosomal protein
45	12	85.7	33	2 PQ0150	dnak-type molecula

ALIGNMENTS

RESULT 1
PA0037
plascocyanin 2 - Arabidopsis thaliana (fragment)
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C/Accession: PA0037
R/Kamo, M.; Kawakami, T.; Miyake, N.; Tsugita, A.
submitted to JRPD, July 1994
A/Description: Separation and characterization of Arabidopsis proteins by two-dimension
A/Reference number: PA0001
A/Accession: PA0037
A/Molecule type: protein
A/Residues: 1-12 <KAM>
A/Experimental source: stem

Query Match
Best Local Similarity 85.7%; Score 12; DB 2; Length 12;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
DB 8 TXY 10

RESULT 2
PC1149
equinotoxin 1A - sea anemone (Actinia equina) (fragment)
C/Species: Actinia equina
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PC1149
R/Komatsu, S.; Furukawa, K.; Abe, K.; Hirano, H.; Ueda, M.
Chem. Pharm. Bull. 40, 2873-2875, 1992
A/Title: Isolation and characterization of equinotoxins from the sea anemone Actinia eq

A/Reference number: PC1149; MUID:93099631; PMID:1361161
A/Accession: PC1149
A/Molecule type: protein
A/Residues: 1-13 <KOM>
C/Keywords: toxin

Query Match
Best Local Similarity 85.7%; Score 12; DB 2; Length 13;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
DB 1 TSY 3

RESULT 3
B39111
ig heavy chain V region - Pacific hagfish (fragment)
C/Species: Eptatretus stouti (Pacific hagfish)

C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C/Accession: B39111
R/Varnier, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A/Title: A serum heterodimer from hagfish (Eptacretus stoutii) exhibits structural simi
C/Species: Aetideus heterodimer from hagfish (Eptacretus stoutii)
A/Reference number: A39111; PMID:9115684; PMID:2000382
A/Accession: B39111
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <VAR>
C/Keywords: heterotetramer; immunoglobulin

Query Match 85.7%; Score 12; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
| |
Db 2 TAY 4

RESULT 4

PH1630
Ig H chain V-D-J region (clone B-less 156) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1630
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A/Reference number: PH1580; PMID:93301609; PMID:8315387
A/Accession: PH1630
A/Molecule type: DNA
A/Residues: 1-17 <LEV>
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 85.7%; Score 12; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
| |
Db 8 TTY 10

RESULT 5

A43826
dnaK-type molecular chaperone - Ajellomyces capsulata (fragment)
N/Alternate names: 80K heat shock protein 70 homolog
C/Species: Ajellomyces capsulata, Histoplasma capsulatum
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C/Accession: A43826
R/Gomez, F.J.; Gomez, A.M.; Deepe UT., G.S.
Infect. Immun. 60, 2565-2571, 1992
A/Title: An 80-kilodalton antigen from Histoplasma capsulatum that has homology to heat
A/Reference number: A43826; PMID:92307875; PMID:1612726
A/Accession: A43826
A/Molecule type: protein
A/Residues: 1-18 <GOM>
A/Cross-references: UNIPROT:Q7M4V0
A/Experimental source: extract of cell wall and cell membrane
C/Function:
A/Description: Involved in protein folding and assembling/disassembling of protein comp
C/Superfamily: heat shock protein 70
C/Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 85.7%; Score 12; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
| |

Db 10 TTY 12

RESULT 6

S70612
alpha-macroglobulin proteinase inhibitor, tetrameric - bloodfluke planorb (fragment)
C/Species: Biomphalaria glabrata (bloodfluke planorb)
C/Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C/Accession: S70612
R/Bender, R.C.; Bayne, C.J.
Biochem. J. 316, 893-900, 1996
A/Title: Purification and characterization of a tetrameric alpha-macroglobulin proteina
A/Reference number: S70612; PMID:96265058; PMID:8670168
A/Accession: S70612
A/Molecule type: protein
A/Residues: 1-18 <BEN>
A/Cross-references: UNIPROT:Q9TWE0
C/Complex: homotetramer
C/Function:
A/Description: inhibits proteinases possessing different catalytic mechanisms by steric

Query Match 85.7%; Score 12; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
| |
Db 15 TAY 17

RESULT 7

PL0025
T-cell surface glycoprotein Rta - rabbit (fragment)
N/Alternate names: thymocyte specific class I-like antigen, heavy chain
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: PL0025
R/Wang, C.R.; Chen, G.H.; Newkirk, M.; Capra, J.D.; Mandy, W.S.
Mol. Immunol. 25, 945-952, 1988
A/Title: Biochemical properties of a novel rabbit thymocyte specific class I-like anti
A/Reference number: PL0025; PMID:89096985; PMID:3264885
A/Accession: PL0025
A/Molecule type: protein
A/Residues: 1-18 <MAN>
A/Cross-references: UNIPROT:Q7M3F4
A/Experimental source: thymus
C/Keywords: glycoprotein; surface antigen

Query Match 85.7%; Score 12; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
| |
| |
Db 8 TSY 10

RESULT 8

PH1783
T cell receptor alpha chain V region (clone 2DN V alpha 24-4) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1783
R/Porcelll, S.; Yockey, C.B.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A/Reference number: PH1754; PMID:93301585; PMID:8391057
A/Accession: PH1783
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-20 <FOR>

Query Match 85.7%; Score 12; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 | |
 | |
 DB 12 TSY 14

RESULT 9

165242 homeotic protein Hox-1 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 16-Aug-2004
 C:Accession: 165242
 R:Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.
 Biochem. Genet. 32: 351-360, 1994
 A>Title: Cloning of rat homeobox genes.
 A:Reference number: 152340; PMID:95217128; PMID:7702549
 A:Accession: 165242
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-20 <RES>
 A:Cross-references: GB:S76293; NID:9913078
 C:Genetics:
 A:Gene: Hox-A; Hox-1
 C:Superfamily: homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 85.7%; Score 12; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 | |
 | |
 DB 6 TSY 8

RESULT 10

S12391 faB protein - Escherichia coli plasmid pFK99 (fragment)
 C:Species: Escherichia coli
 C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C:Accession: S12391
 R:Simons, B.L.; Willemsen, P.T.J.; Bakker, D.; Roosendaal, B.; de Graaf, F.K.; Oudega, H.
 Mol. Microbiol. 4: 2041-2050, 1990
 A>Title: Structure, localization and function of faB, a minor component of K99 fibrillin
 A:Reference number: S12391; PMID:91211613; PMID:1982454
 A:Accession: S12391
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <SIM>
 A:Cross-references: UNIPROT:P25402
 C:Genetics:
 A:Gene: faB
 A:Genome: plasmid pFK99

Query Match 85.7%; Score 12; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 | |
 | |
 DB 14 TSY 16

RESULT 11

B42382 replication initiation protein RepA - Escherichia coli plasmid pMU720 (fragment)
 C:Species: Escherichia coli
 C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 17-Feb-1994
 C:Accession: B42382
 R:Praschler, J.; Wilson, I.W.; Pittard, A.J.

J. Bacteriol. 174: 2276-2383, 1992
 A>Title: Mutations affecting translational coupling between the rep genes of an IncB pl
 A:Reference number: A42382; PMID:92202169; PMID:1372603
 A:Accession: B42382
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-23 <PRA>
 A:Cross-references: GB:M33063; GB:M38522
 C:Genetics:
 A:Genome: plasmid

Query Match

85.7%; Score 12; DB 2; Length 23;
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 | |
 | |
 DB 7 TSY 9

RESULT 12

PH1713 Ig heavy chain V region (clone ASC-11) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
 C:Accession: PH1713
 R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
 J. Exp. Med. 178: 295-307, 1993
 A>Title: Antigen-driven B cell differentiation in vivo.
 A:Reference number: PH1675; PMID:93301607; PMID:8315385
 A:Accession: PH1713
 A:Molecule type: mRNA
 A:Residues: 1-24 <MCH>
 A:Experimental source: B cell
 A>Note: the authors translated GTA for residue 11 as Thr and ACA for residue 13 as Ala
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 85.7%; Score 12; DB 2; Length 24;
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 | |
 | |
 DB 13 TSY 15

RESULT 13

PH1712 Ig heavy chain V region (clone ASC-10) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
 C:Accession: PH1712
 R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
 J. Exp. Med. 178: 295-307, 1993
 A>Title: Antigen-driven B cell differentiation in vivo.
 A:Reference number: PH1675; PMID:93301607; PMID:8315385
 A:Accession: PH1712
 A:Molecule type: mRNA
 A:Residues: 1-24 <MCH>
 A:Experimental source: B cell
 A>Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 85.7%; Score 12; DB 2; Length 24;
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 | |
 | |
 DB 13 TSY 15

RESULT 14

B27262
 nicotinic acetylcholine receptor beta chain - electric eel (fragment)
 C/Species: Electrophorus electricus (electric eel)
 C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
 C/Accession: B27262
 R/Conti-Tironconi, B.M.; Hunkapiller, M.W.; Lindstrom, J.M.; Raftery, M.A.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6489-6493, 1982
 A/Title: Subunit structure of the acetylcholine receptor from Electrophorus electricus.
 A/Reference number: A93932; PMID:83065199; PMID:6959131
 A/Accession: B27262
 A/Molecule type: protein
 A/Residues: 1-24 <CON>
 A/Cross-references: UNIPROT:P03689
 C/Keywords: glycoprotein; ion channel; membrane protein; neurotransmitter receptor; post

Query Match

Best Local Similarity 85.7%; Score 12; DB 2; Length 24;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 11 TSY 13

RESULT 15

JH0701
 omega-conotoxin MVIR - cone shell (Conus magus)
 C/Species: Conus magus (magus cone)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C/Accession: JH0701; B34115
 R/Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; M
 Neuron 9, 69-77, 1992
 A/Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.
 A/Reference number: JH0699; PMID:92337922; PMID:1352986
 A/Accession: JH0701
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-25 <HIL>
 A/Cross-references: UNIPROT:P05485
 R/Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.;
 Biochemistry 26, 2086-2090, 1987
 A/Title: Neuronal calcium channel antagonists. Discrimination between calcium channel su
 A/Reference number: A34115; PMID:87299637; PMID:2441741
 A/Accession: B34115
 A/Molecule type: protein
 A/Residues: 1-25 <OLI>
 C/Superfamily: omega-conotoxin
 C/Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh
 F/1-16, 8-20, 15-25/Disulfide bonds; #status predicted
 F/25/Modified site: amidated carboxyl end (Cys) #status predicted

Query Match

Best Local Similarity 85.7%; Score 12; DB 2; Length 25;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 11 TSY 13

Search completed: December 13, 2004, 22:33:01
 Job time : 17.2 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 22:00:41 ; Search time 83.8 Seconds

(without alignments)
27.464 Million cell updates/sec

Title: US-10-068-905-9

Sequence: 1 TXX 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	85.7	9	2	Q9BYF9
2	12	85.7	9	2	Q70Y80
3	12	85.7	9	2	CAD45507
4	12	85.7	10	2	Q94186
5	12	85.7	12	2	Q70Y60
6	12	85.7	13	2	CAD45540
7	12	85.7	13	2	Q818F3
8	12	85.7	13	2	Q7BVK6
9	12	85.7	14	2	Q6ZYT7
10	12	85.7	14	2	Q8RK22
11	12	85.7	14	2	CAG24647
12	12	85.7	15	1	UC19_WAIZ
13	12	85.7	15	1	Q6SLH8
14	12	85.7	15	2	Q6ZYT6
15	12	85.7	15	2	Q6ZYT6
16	12	85.7	15	2	CAG24649
17	12	85.7	16	2	Q7JFY3
18	12	85.7	16	2	Q98898
19	12	85.7	17	2	Q06800
20	12	85.7	17	2	Q6CWS6
21	12	85.7	17	2	Q6ZYT4
22	12	85.7	17	2	CAG24652
23	12	85.7	17	2	Q6ZYT4
24	12	85.7	17	2	Q6ZYT4
25	12	85.7	17	2	Q6ZYT4
26	12	85.7	17	2	Q6ZYT4
27	12	85.7	17	2	Q6ZYT4
28	12	85.7	17	2	Q6ZYT4
29	12	85.7	17	2	Q6ZYT4
30	12	85.7	17	2	Q6ZYT4
31	12	85.7	17	2	Q6ZYT4

32	12	85.7	17	2	AAP69438	AAP69438 trochoden
33	12	85.7	17	2	AAP69439	AAP69439 trochoden
34	12	85.7	17	2	AAP69440	AAP69440 trochoden
35	12	85.7	17	2	AAP69441	AAP69441 trochoden
36	12	85.7	17	2	AAP69442	AAP69442 trochoden
37	12	85.7	17	2	AAP69443	AAP69443 trochoden
38	12	85.7	17	2	AAP69444	AAP69444 trochoden
39	12	85.7	17	2	AAP69445	AAP69445 trochoden
40	12	85.7	17	2	AAP69446	AAP69446 trochoden
41	12	85.7	17	2	AAP69447	AAP69447 trochoden
42	12	85.7	17	2	AAP69448	AAP69448 trochoden
43	12	85.7	17	2	AAP69449	AAP69449 trochoden
44	12	85.7	17	2	AAP69450	AAP69450 trochoden
45	12	85.7	17	2	AAP69451	AAP69451 trochoden

ALIGNMENTS

RESULT 1

Q9BYF9 PRELIMINARY; PRT; 9 AA.

AC Q9BYF9, 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

SEQUENCE FROM N.A.

RP MEDLINE=21539745; PubMed=11682035;

RA Kagaya M., Kaneko S., Ohno H., Inamura K., Kobayashi K.;

RT "Cloning and characterization of the 5'-flanking region of human

RL J. Hepatol. 35:504-511 (2001).

DR EMBL; AB045973; BAB40770.1; "

DR GO; GO:0005882; C:Intermediate filament; IEA.

KW Keratin.

FT NON TER.

SO SEQUENCE

Query Match

Best Local Similarity 66.7%; Pred. No. 1.8e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXX 3

DB 2 TSY 4

RESULT 2

Q70Y80 PRELIMINARY; PRT; 9 AA.

AC Q70Y80, 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

GN Ribosomal protein (Fragment).

OC Chloroplast; Viridiplantae; Streptophyta; Tracheophyta;

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Lamiales; Lamiaceae; Nepentidae; Ocimeae; Plectranthus.

NCBI_TaxID=204187;

SEQUENCE FROM N.A.

RP PubMed=15019625;

RX PubMed=15019625;

Paton A., Springate D.A., Sudd S., Ocleno D., Grayer R., Harley M.M.;

RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
 based on three plastid DNA regions.";
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL; AJ505387; CAD45507.1;
 GO GO:0003735; P:structural constituent of ribosome; IEA.
 KM Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1053 MW; 6363D1B845A1A33B CRC64;

Query Match 85.7%; Score 12; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 DB 4 TSY 6

RESULT 3

CAD45507 PRELIMINARY; PRT; 9 AA.
 ID CAD45507
 AC CAD45507
 DT 14-MAR-2004 (TREMBlrel. 27, Created)
 DT 14-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DE Ribosomal protein (Fragment).
 GN RPS16.
 OS Pleocanthus glabratus.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiales; Lamiales; Nepentodeae; Ocimeae; Flectranthus.
 OC NCB1_TaxID=204187;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paton A., Springate D.A., Sude S., Otiemo D., Grayer R., Harley M.M.,
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
 based on three plastid DNA regions.";
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL; AJ505387; CAD45507.1;
 GO GO:0003735; P:structural constituent of ribosome; IEA.
 KM Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1053 MW; 6363D1B845A1A33B CRC64;

Query Match 85.7%; Score 12; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 DB 4 TSY 6

RESULT 4

Q941S6 PRELIMINARY; PRT; 10 AA.
 ID Q941S6
 AC Q941S6
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE Nonspecific lipid transfer protein (Fragment).
 OS Pinus taeda (lobolly pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiales; Lamiales; Nepentodeae; Ocimeae; Pinaceae; Pinus.
 OC NCB1_TaxID=3352;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jones D.F.;
 RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY029012; AAK40261.1; --
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1099 MW; 282C1E3B41B1AE7 CRC64;
 Query Match 85.7%; Score 12; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.2e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 DB 5 TTY 7

RESULT 5

O70Y60 PRELIMINARY; PRT; 12 AA.
 ID O70Y60
 AC O70Y60
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Ribosomal protein (Fragment).
 GN Name=rps16;
 OS Ocimum x citridorum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiales; Lamiales; Nepentodeae; Ocimeae; Ocimum.
 OC NCB1_TaxID=204098;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paton A., Springate D.A., Sude S., Otiemo D., Grayer R., Harley M.M.,
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
 based on three plastid DNA regions.";
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL; AJ505420; CAD45540.1;
 GO GO:0003735; P:structural constituent of ribosome; IEA.
 KM Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1264 MW; C4F8FBC776C41772 CRC64;

Query Match 85.7%; Score 12; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 3.8e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 DB 1 TSY 3

RESULT 6

CAD45540 PRELIMINARY; PRT; 12 AA.
 ID CAD45540
 AC CAD45540
 DT 14-MAR-2004 (TREMBlrel. 27, Created)
 DT 14-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DE Ribosomal protein (Fragment).
 GN RPS16.
 OS Ocimum x citridorum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiales; Lamiales; Nepentodeae; Ocimeae; Ocimum.
 OC NCB1_TaxID=204098;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paton A., Springate D.A., Sude S., Otiemo D., Grayer R., Harley M.M.,
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
 based on three plastid DNA regions.";

MoL. Phylogenet. Evol. 31:277-299 (2004).
 DR EMBL; AJ505420; CAD45540.1; -
 KW Chloroplast; Ribosomal protein.
 FT NON TER
 SQ SEQUENCE 12 AA, 1264 MW, C4F8FBC77C641772 CRC64;

Query Match 85.7%; Score 12; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 3.8e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 DB 1 TSY 3

RESULT 7

Q818F3 PRELIMINARY; PRT; 13 AA.
 AC Q818F3; 01-VAR-2003 (TREMBlrel. 23, Created)
 DT 01-VAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-VAR-2003 (TREMBlrel. 24, Last annotation update)
 DE Acetylcholinesterase (Fragment).
 GN Name=Ace; Synonyms=ache;
 OS Drosophila parisiensis.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila; mayaguana subcluster.
 OX NCBI_TaxID=214822;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Grady P.M., Durando C.M., Heed W.B., Wasserman M., Eiges W.,
 RA Desalle R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY154986; AA013634.1; -
 DR FlyBase; FBgn0064412; DpSlVAc.
 FT NON TER
 SQ SEQUENCE 13 AA, 1451 MW, 67DAF26C3079B774 CRC64;
 Query Match 85.7%; Score 12; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 4.1e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 DB 11 TSY 13

RESULT 8

Q7BVK6 PRELIMINARY; PRT; 13 AA.
 AC Q7BVK6; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Streptomycin resistance protein B (Fragment).
 GN Name=StrB;
 OS Erwinia amylovora.
 OG Plantia; Prokaryota; Gammaproteobacteria; Enterobacteriales;
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Erwinia.
 OX NCBI_TaxID=552;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CA3R;
 RX MEDLINE=98027397; PubMed=9361446;
 RA Palmer B.L., Tevordale B.L., Jones A.L.;
 RL "A relative of the broad-host-range plasmid RSF1010 detected in
 RT Erwinia amylovora".
 RT Appl. Environ. Microbiol. 63:4604-4607 (1997).
 DR EMBL; AF017390; AAC45878.1; -

KW Plasmid.
 FT NON TER
 SQ SEQUENCE 13 AA, 1449 MW, 5638FAE39B3FD6D3 CRC64;

Query Match 85.7%; Score 12; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 4.1e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 DB 11 TSY 13

RESULT 9

O6ZYT7 PRELIMINARY; PRT; 14 AA.
 AC O6ZYT7; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Cycochrome b6/f complex subunit VI (Fragment).
 GN Name=petL;
 OS Silene uralensis.
 CC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=269082;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Popp M.;
 RL "Disentangling the reticulate history of polyploids in Silene
 (Caryophyllaceae)".
 RL Thesis (2004), Department of Evolutionary Biology, Systematic Botany,
 RL Uppsala University, Uppsala, Sweden.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Popp M., Erikson P., Eggens F., Oxelman B.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ544219; CAG24647.1; -
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 14 AA, 1532 MW, 06428D1B688740DB CRC64;

Query Match 85.7%; Score 12; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 4.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TXY 3
 DB 5 TSY 7

RESULT 10

O8RK22 PRELIMINARY; PRT; 14 AA.
 AC O8RK22; 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Transposase (Fragment).
 GN Name=tnpA;
 OS Pseudomonas fluorescens.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TC29-5;
 RX MEDLINE=22315381; PubMed=12427948;

RA Kholodil G., Gorlenko Z., Mindlin S., Hobman J., Nikiforov V.;
 "un5041-like transposons: molecular diversity, evolutionary
 RT relationships and distribution of distinct variants in environmental
 RT bacteria";
 RL Microbiology 148:3569-3582(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TC29-5;
 RA Kholodil G.Y.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY422232; CAD19590.1; -
 PT NON_TER 14
 SQ SEQUENCE 14 AA; 1535 MW; 866834BEP82164C1 CRC64;
 QY Query Match 85.7%; Score 12; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 4.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 TRY 3
 7 TRY 9

RESULT 11
 CAG24647 PRELIMINARY; PRT; 14 AA.
 ID CAG24647
 AC CAG24647
 DT 31-MAR-2004 (TREMBlrel. 27, Created)
 DT 31-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 31-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Cytochrome b6/f complex subunit VI (Fragment).
 GN PTL.
 OS Silene uraleensis.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=269082;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Popp M., Erikson P., Eggens F., Oxelman B.;
 RL "Origin and evolution of a circumpolar polyploid species complex in
 RT Silene (Caryophyllaceae).";
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Popp M.;
 RL "Disentangling the reticulate history of polyploids in Silene
 RT (Caryophyllaceae).";
 RL Thesis (2004), Department of Evolutionary Biology, Systematic Botany,
 RU Uppsala university, Uppsala, Sweden.
 DR EMBL: AY634219; CAG24647.1; -
 KW Chloroplast.
 PT NON_TER 14
 SQ SEQUENCE 14 AA; 1532 MW; 06428D1B688740DB CRC64;
 QY Query Match 85.7%; Score 12; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 4.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 TRY 3
 5 TRY 7

RESULT 12
 UC19_MAIZE STANDARD; PRT; 15 AA.
 ID UC19_MAIZE
 AC P80625;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 406)
 DE (Fragment)
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=coleoptile;
 RA Tournet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Fernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RL genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.6, its MW is: 18.4 KDa.
 DR Maize-2DPAGE: P80625; COLEOPTILE.
 DR MaizeDB: 123951; -
 FT NON_TER 15
 PT NON_TER 15
 SQ SEQUENCE 15 AA; 1672 MW; 1CF69DAD8737F9D CRC64;
 QY Query Match 85.7%; Score 12; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 TRY 3
 6 TRY 8

RESULT 13
 Q6SLH8 PRELIMINARY; PRT; 15 AA.
 ID Q6SLH8
 AC Q6SLH8;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE UORP2.
 GN Name=gna-2;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Rhabditinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee M.-H., Schedl T.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY455927; AAR26306.1; -
 KW Rhabditidae.
 PT NON_TER 15
 SQ SEQUENCE 15 AA; 1901 MW; 86D1593EFA18C498 CRC64;
 QY Query Match 85.7%; Score 12; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 TRY 3
 8 TRY 10

RESULT 14
 Q6ZYT6 PRELIMINARY; PRT; 15 AA.
 ID Q6ZYT6
 AC Q6ZYT6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Cytochrome b6/f complex subunit VI (Fragment).
 GN Name=petl;
 OS Silene uraleensis.

OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=269082;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=leaf;
 RA Popp M.;
 RT "Disentangling the reticulate history of polyploids in Silene
 Thesis (2004), Department of Evolutionary Biology, Systematic Botany,
 RL Uppsala university, Uppsala, Sweden.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=leaf;
 RA Popp M., Erickson P., Eggens F., Oxelman B.;
 RU Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AJ634220; CAG24649.1;
 DR GO; GO:0009507; C:Chloroplast; IEA.
 KM Chloroplast.
 FT NON TER
 SQ SEQUENCE 15 AA; 1645 MW; C716428D1B68740 CRC64;

Query Match 85.7%; Score 12; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TXY 3
 Db 5 TSY 7

RESULT 15
 ID AAR26306 PRELIMINARY; PRT; 15 AA.
 AC AAR26306;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE UORP2.
 GN GNA-2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee M.-H., Schedl T.;
 RT "translational repression by GLD-1 protects its mRNA targets from non-
 sense mediated mRNA decay." to the EMBL/GenBank/DBJ databases.
 RL Submitted (OCT-2003)
 DR EMBL, AY455927; AAR26306.1; -
 SQ SEQUENCE 15 AA; 1901 MW; 86D1593EFA18C498 CRC64;

Query Match 85.7%; Score 12; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TXY 3
 Db 8 TSY 10

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